

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 21, 2001, 20:57:45 ; Search time 24.5 Seconds  
(Without alignments)  
1981.875 Million cell updates/sec

Title: US-09-575-061-1  
Perfect score: 1953  
Sequence: 1 MKSKVLLALLPALLAAGAAH.....TRDAGINTDVALGLVYQF 367

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues  
Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SPREMBL\_16:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_unclassified:\*  
13: sp\_vertebrate:\*  
14: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1787.5	91.5	366	2	Q9RH85
2	1709.5	87.5	364	2	Q9K597
3	1534.5	78.6	378	2	Q9K3E6
4	1296	66.4	377	2	Q85030
5	1250.5	64.0	374	2	Q87754
6	1025.5	52.5	363	2	Q9K3E7
7	1018.5	52.2	333	2	Q9RAW3
8	1018.5	52.2	333	2	Q9RAW2
9	1015.5	52.0	333	2	Q9S613
10	1015.5	52.0	360	2	Q9F889
11	1010.5	51.7	333	2	Q9R859
12	1009.5	51.7	339	2	Q87753
13	862.5	44.2	315	2	Q9EXH8
14	732	37.5	315	2	Q9ZC71
15	518.5	26.5	130	2	Q52641
16	314	16.1	351	2	Q9RNA1
17	310	15.9	96	2	P77519
18	296	15.2	111	2	P94857
19	296	15.2	111	2	P94858

20	296	15.2	111	2	P94860	P94860 klebsiella
21	288	14.7	111	2	P94635	P94635 calymmatoba
22	257	13.2	69	2	P76871	P76871 escherichia
23	254	13.0	331	2	Q9KKU2	Q9KKU2 vibrio chol
24	232.5	11.9	356	2	Q9KH07	Q9KH07 aeromonas h
25	198.5	10.2	357	2	Q01452	Q01452 haemophilus
26	174.5	8.9	357	2	Q48225	Q48225 haemophilus
27	174.5	8.9	357	2	Q68631	Q68631 haemophilus
28	174	8.9	343	2	Q54340	Q54340 pasteurella
29	174	8.9	361	2	Q68624	Q68624 haemophilus
30	173.5	8.9	378	2	Q01451	Q01451 haemophilus
31	173	8.9	360	2	Q68626	Q68626 haemophilus
32	171	8.8	333	2	Q54339	Q54339 pasteurella
33	169	8.7	50	2	Q9ZC72	Q9ZC72 yersinia pe
34	169	8.7	360	2	Q68623	Q68623 haemophilus
35	168.5	8.6	361	2	Q45106	Q45106 burkholderi
36	168.5	8.6	363	2	Q68628	Q68628 haemophilus
37	168.5	8.6	368	2	Q68633	Q68633 haemophilus
38	167.5	8.6	374	2	Q05107	Q05107 ectothiorho
39	167	8.6	328	2	Q54347	Q54347 pasteurella
40	166	8.5	364	2	Q68627	Q68627 haemophilus
41	166	8.5	328	2	Q54349	Q54349 pasteurella
42	165.5	8.5	364	2	Q68632	Q68632 haemophilus
43	165	8.4	330	2	P94743	P94743 eikenella c
44	164	8.4	346	2	Q52639	Q52639 neisseria g
45	163	8.3	348	2	Q08266	Q08266 neisseria g

## ALIGNMENTS

RESULT 1  
ID Q9RH85 PRELIMINARY; PRT; 366 AA.  
AC Q9RH85;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN OMPC.  
GN OMPC.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=O157:H7;  
RA Yu S.L., Syu W.J.;  
RT "Altered outer membrane protein OmPC in hemorrhagic Escherichia coli O157:H7."  
RT Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE (BY SIMILARITY).  
CC EMBL: AF057355; AAF21761.1; -.  
DR HSSP: Q48473; IOSM.  
DR InterPro: IPR001702; -.  
DR Pfam: PF00267; Gram-ve\_porins; 1.  
DR PRINTS: PR00182; ECOLNEIPORIN.  
DR PROSITE: PS00576; GRAM\_NEG\_PORIN; 1.  
KW Outer membrane; Porin; Signal; Transmembrane.  
SQ SEQUENCE 366 AA; 40499 MW; 6A4EADI652565C00 CRC64;

Query Match 91.5%; Score 1787.5; DB 2; Length 366;  
Best Local Similarity 91.6%; Pred. No. 1.1e-118;  
Matches 340; Conservative 9; Mismatches 13; Indels 9; Gaps 2;

OY 1 MKSKVLLALLPALLAAGAAHAEYNNKDKGLDYGKVDGLHFSDDKVDGQOTYRLG 60  
DB 1 MKKAVLSLVPALLVAGAAHAEYNNKDKGLDYGKVDGLHFSDDKSVGQOTYRLG 60  
OY 61 FKGETVTDLTGCGWEYOIGNSAENENNSWTRVAFGLKFDVGSPDYGRNYGVYD 120

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Db      61 FKQETVTDLDTGYGMEYOIOGNSAENENSWTRAFAPLAKQDVGSFPGYGRNYGYVD 120
      121 VTSMTDVLPEFGDDTYGSDNFMQOQNGNFATYRNTPDFGLVDGLNFAVOYQKNGNPSGE 180
      121 VTSMTDVLPEFGDDTYGSDNFMQOQNGNFATYRNTPDFGLVDGLNFAVOYQKNGNPSGE 178
      181 GFTSGVTNNGRDALRQNGDVGSGITTYDEGFGIGAISSSKRPDQONTAAIYGNDRAE 240
      179 ---EGMTNNGREALRQNGDVGSGITTYDEGFGIGAAVSSSKRTDDQNSPLYIGNGRAE 235
      241 TTYTGKLYDANNITYLAAOYTQTNATRVGSLGNANKQNEEAAVOXQOFDGLRPSLAYLQ 300
      236 TTYTGKLYDANNITYLAAOYTQTNATRVGSLGNANKQNEEAAVOXQOFDGLRPSLAYLQ 295
      301 SKGKNL----GRGYDEDDILKYVDGATYTFNKNMSTYVDYKINLDDNQFTRDAGINTD 356
      296 SKGKNLGVINGRYNDEDDILKYVDGATYTFNKNMSTYVDYKINLDDNQFTRDAGINTD 355
      357 NIVALGLVYQF 367
      356 NIVALGLVYQF 366

RESULT 2
ID      09K597      PRELIMINARY:      PRT:      364 AA.
AC      09K597;
DT      01-OCT-2000 (TREMBLrel. 15, Created)
DT      01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT      01-MAR-2001 (TREMBLrel. 16, last annotation update)
DE      OUTER MEMBRANE PORIN C PRECURSOR.
GN      OMP.
OS      Escherichia coli.
OC      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OX      Escherichia.
OX      NCBI_Taxid=562;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      LOW A.S., Mackenzie F.M., Gould I.M., Booth I.R.;
RT      "Parallel evolution of multi-resistant bacteria in a patient with
RT      recurrent septicemia: unique data that support the presence of
RT      separate protected environments."
RL      Submitted (AUG-2000) to the EMBL/Genbank/DBJ databases.
CC      -1- SUBUNIT: HOMOMER (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE
CC      (BY SIMILARITY).
DR      EMBL; AJ295721; CAC01403.1; -
DR      InterPro; IPR000504; -
DR      InterPro; IPR001702; -
DR      Pfam; PF00267; Gram-ve_porins; 1.
DR      PRINTS; PR00182; ECOLNEIPORIN.
DR      PROSITE; PS00576; GRAM_NEG_PORIN; 1.
DR      PROSITE; PS00030; RNP_1; UNKNOWN_1.
KW      Outer membrane; Porin; Signal; Transmembrane.
FT      SIGNAL 1 21 POTENTIAL.
FT      CHAIN 364 AA; 40312 MW; 9B583FC1344E31 CRC64;
SQ      SEQUENCE

Query Match      87.5%; Score 1709.5; DB 2; Length 364;
Best Local Similarity 88.0%; Pred. No. 3.4e-113;
Matches 333; Conservative 14; Mismatches 27; Indels 3; Gaps 1;

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Db      121 VTSMTDVLPEFGDDTYGSDNFMQOQNGNFATYRNTPDFGLVDGLNFAVOYQKNGNPSGE 180
      181 GFTSGVTNNGRDALRQNGDVGSGITTYDEGFGIGAISSSKRTDQONTAAIYGNDRAE 240
      181 GMT---TNGRDVDFEONGDVGSGITTYDEGFGIGAAVSSSKRTDQONTNGLTGTDRAE 237
      241 TTYTGKLYDANNITYLAAOYTQTNATRVGSLGNANKQNEEAAVOXQOFDGLRPSLAYLQ 300
      238 TTYTGKLYDANNITYLAAOYTQTNATRVGSLGNANKQNEEAAVOXQOFDGLRPSLAYLQ 297
      301 SKGKNLGRGYDEDDILKYVDGATYTFNKNMSTYVDYKINLDDNQFTRDAGINTDIVA 360
      298 SKGKNLGRGYDEDDILKYVDGATYTFNKNMSTYVDYKINLDDNQFTRDAGINTDIVA 357
      361 LGLVYQF 367
      358 LGLVYQF 364

RESULT 3
ID      09K3E6      PRELIMINARY:      PRT:      378 AA.
AC      09K3E6;
DT      01-OCT-2000 (TREMBLrel. 15, Created)
DT      01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT      01-MAR-2001 (TREMBLrel. 16, last annotation update)
DE      OUTER MEMBRANE PROTEIN C PRECURSOR.
GN      OMP.
OS      Salmonella enterica subsp. enterica serovar Minnesota.
OC      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OX      Salmonella.
OX      NCBI_Taxid=70803;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      STRAIN-SF111;
RA      Zimmermann H., Wassenaar T.M., Laubenhilner-Preusse H., Petry F.,
RA      Loois M.;
RL      Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.
CC      -1- SUBUNIT: HOMOMER (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE
CC      (BY SIMILARITY).
DR      EMBL; Y15844; CAB96613.1; -
DR      InterPro; IPR000504; -
DR      InterPro; IPR001702; -
DR      Pfam; PF00267; Gram-ve_porins; 1.
DR      PRINTS; PR00182; ECOLNEIPORIN.
DR      PROSITE; PS00576; GRAM_NEG_PORIN; 1.
DR      PROSITE; PS00030; RNP_1; UNKNOWN_1.
KW      Outer membrane; Porin; Signal; Transmembrane.
FT      SIGNAL 1 21 POTENTIAL.
FT      CHAIN 378 378 OUTER MEMBRANE PROTEIN C.
FT      CHAIN 378 378 OUTER MEMBRANE PROTEIN C.
SQ      SEQUENCE 378 AA; 41269 MW; 254524EB9EC3849C CRC64;

Query Match      78.6%; Score 1534.5; DB 2; Length 378;
Best Local Similarity 77.1%; Pred. No. 8e-101;
Matches 296; Conservative 25; Mismatches 40; Indels 23; Gaps 5;

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Db 62 GFGKGETOINTDLTGFQWMEKRTKADRAEGEQNSNLVRLAFAGLKAEVGSIDYGRNYGI 121
118 VYVTSWTDVLPREGGTYG---SDNPMOQRGNFGATYRNTDFEGVLDGLENFAVOYQGN 124
122 VYVTSWTDVLPREGGTYG---SDNPMOQRGNFGATYRNTDFEGVLDGLENFAVOYQGN 121
175 GNSGEGFTSGVYNNRDLRONGDVGSGITVDYEGFISGAISSSKRTDQNTAAYIG 234
182 -----QDNHSINSQNGDGYTMAIEFDGFGVTAAYNSKRTNDQDNR--G 226
QY 235 NGDRAETTYGCLKYDANNIYLAAYQTYNA-----TRVSLGMANKAONEAAYOYQFD 289
227 NGDRASMAWAGAKYDANNIYLAAYVETRNMSIVENTVDTVEAMANKTONLEVAAYOYQFD 286
QY 290 EGLRPSLAYOSKGNLGRYDDEDLKYVDGATYFNNKMSITYDYKINLDDNQFTFR 349
287 EGLRPAISTYQSKGNLNGADGSDADLAKYIQAGATYFNNKMSIVENTVDTVEAMANKTONLEVAAYOYQFD 345
Db 350 DAGINTDNIALGLV 364
QY 346 SSVYGTDDQAAVGI 360
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RESULT 11
Q9RS9 PRELIMINARY: PRT: 333 AA.
AC 09RS9:
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE PHOSPHATE PORIN (FRAGMENT).
GN
OS Calymmatobacterium granulomatis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Calymmatobacterium.
NCBI_Taxid=39824;
RN
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20023050; PubMed=1055350;
RA Carter J.S., Bowden F.J., Bastian I., Myers G.M., Sripaksh K.S.,
Kemp D.J.;
RT "Phylogenetic evidence for reclassification of Calymmatobacterium
granulomatis as Klebsiella granulomatis comb. nov."
RL Int. J. Syst. Bacteriol. 49:1695-1700(1999).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE
(CY SIMILARITY).
CC EMBL: AF009231; MAD21519.1; -.
DR HSSP: P02932; IPHO.
DR InterPro: IPR001702; -.
DR Pfam: PF00267; Gram-ve_porins; 1.
DR PRINTS: PR00182; ECOLIETPORIN.
DR PROSITE: PS00576; GRAM_NEG_PORIN; 1.
FT Outer membrane; Porin; Signal; Transmembrane.
FT NON_TER 1 1
FT NON_TER 333 333
SQ SEQUENCE 333 AA; 36786 MW; 7CEA2F68B998BB0A CRC64;
```

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Query Match 51.7%; Score 1010.5; DB 2; Length 333;
Best Local Similarity 56.2%; Pred. No. 6; 6e-64;
Matches 199; Conservative 53; Mismatches 77; Indels 25; Gaps 8;
QY 8 LIPALLAAGAAHAAYNNKDKKLDLYGKVDGLHFSDNKDVGDQTYRKLFGKGETOY 67
1 LMMGVASTATQAAEYNNKANKLDYGRKIMHFSDDSKDGOYVRFGIKETOI 60
Db 68 TDOLTYGWEYIOGNSAENENNSWTRVAFALGFQDVGSGFYGRNYGVVYVTSWTDV 127
1 TDOLTYGWEYIOGNSAENENNSWTRVAFALGFQDVGSGFYGRNYGVVYVTSWTDV 127
Db 61 NDLDTYGRSEFSGKRTSDSSQKTRLAFAVKLAKNGSPFYGRNLGALIVYEMATDM 120
128 LPBFGDITYG-SDNPMOQRGNFGATYRNTDFGLVDGLNFAVOYQGNPSGEGFTSGV 186
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Db 121 FPFEGDSSAQDTNFMWKTRASGLATYRNTDFGLVGLDLTLQYQK----- 167
187 TNGRGRALRONGGCGVGSITYDEG--FGIGAISSSKRTDQNTAAYIGNGDRAETTYG 244
168 -NEGCEKKNKONGCGVGSITYDEGSDPFAASAATYSSDRNDQNLAR-GQSKAANAT 225
QY 245 GLKYDANNIYLAAYQTYNATRVGSLGNANKAONEAAYOYQFDGLRPSLAYOSKGR 304
226 GLKYDANNIYLAAYVETRNMSIVENTVDTVEAMANKTONLEVAAYOYQFDGLRPSLAYOSKGR 284
QY 305 NGRGYDDEDLKYVDGATYFNNKMSITYDYKINLDDNQFTDAGINTDN 357
285 DI-EGVGSIEDLVNYIDVGLTYFNNKMSIVENTVDTVEAMANKTONLEVAAYOYQFDGLRPSLAYOSKGR 333
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RESULT 12
087753 PRELIMINARY: PRT: 359 AA.
AC 087753:
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE OMPK35 PORIN PRECURSOR.
GN
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
NCBI_Taxid=573;
RN
[1]
RP SEQUENCE FROM N.A.
RX STRAIN=KT755;
RA Hernandez-Alles S.;
RL Thesis (1998), Universitat de les Illes Balears, Valencia, Spain.
DR EMBL: A011501; CA09365.1; -.
DR HSSP: P02931; IGFN.
DR InterPro: IPR001702; -.
DR Pfam: PF00267; Gram-ve_porins; 1.
DR PRINTS: PR00182; ECOLIETPORIN.
KW Signal.
FT SIGNAL 1 22
FT CHAIN 23 359
FT POTENTIAL.
FT OMPK35 PORIN.
SQ SEQUENCE 359 AA; 39510 MW; 12D5183400585BB CRC64;
```

```
Query Match 51.7%; Score 1009.5; DB 2; Length 359;
Best Local Similarity 53.5%; Pred. No. 8; 6e-64;
Matches 200; Conservative 54; Mismatches 97; Indels 23; Gaps 6;
```

```
QY 1 MKSKVALLIPALLAAGAAHAAYNNKDKKLDLYGKVDGLHFSDNKDVGDQ-TYMR 59
2 MKRNIILAVIPALLVAGAAHAAYNNKDKKLDLYGKVDGLHFSDNKDVGDQ-TYMR 61
QY 60 GFGKGETOINTDLTGFQWMEKRTKADRAEGEQNSNLVRLAFAGLKAEVGSIDYGRNYGI 119
62 GFGKGETOINTDLTGFQWMEKRTKADRAEGEQNSNLVRLAFAGLKAEVGSIDYGRNYGI 121
QY 120 DYSWTDVLPREGGTYG---SDNPMOQRGNFGATYRNTDFEGVLDGLENFAVOYQGN 178
122 DYSWTDVLPREGGTYG---SDNPMOQRGNFGATYRNTDFEGVLDGLENFAVOYQGN 178
Db 122 DYSWTDVLPREGGTYG---SDNPMOQRGNFGATYRNTDFEGVLDGLENFAVOYQGN 178
179 GEGFTSGVYNNRDLRONGDVGSGITVDYEGFISGAISSSKRTDQNTAAYIG 237
178 -----DHRATRKQNGDGSSTATYAFDNGIALSGYSSNNNSVDQKND---GND 225
QY 238 RAETTYGCLKYDANNIYLAAYQTYNATRVGSLGNANKAONEAAYOYQFDGLRPSLA 297
226 KAEMATSAKYDANNIYLAAYVETRNMSIVENTVDTVEAMANKTONLEVAAYOYQFDGLRPSLA 285
QY 298 YLOSCKNLT-----GRGYDDEDLKYVDGATYFNNKMSITYDYKINLDDNQFTDAGI 353
286 YVOTKGRDQLQSRAGSGADLVKLTVEGTWYFNNKMSIVENTVDTVEAMANKTONLEVAAYOYQFDGLRPSLA 345
```

OY 354 NMDNVALGLYOF 367  
 DB 346 ATDDAAVGIYOF 359

## RESULT 13

O9EXH8 PRELIMINARY; PRT; 315 AA.  
 AC O9EXH8;  
 DT 01-MAR-2001 (Tremblrel, 16, Created)  
 DT 01-MAR-2001 (Tremblrel, 16, Last sequence update)  
 DT 01-MAR-2001 (Tremblrel, 16, Last annotation update)  
 DE OMPK35 PROTEIN PRECURSOR.  
 GN OMPK35.  
 OS Klebsiella pneumoniae.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Klebsiella.  
 OX NCBI\_TaxID=573;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-103624;  
 RA Crowley B., Benedi V.J., Domenech-Sanchez A.;  
 RT "Expression of altered ompK35 porin and SHY-2 beta-lactamase in  
 Klebsiella pneumoniae results in cephalosporins and carbapenems  
 resistance."  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ303057; CAC18650.1;  
 KW Signal.  
 FT SIGNAL. 1 22 POTENTIAL.  
 FT CHAIN 23 315 OMPK35 PROTEIN.  
 SQ SEQUENCE 315 AA; 34420 MW; F45748383475D8CA CRC64;

Query Match 44.2%; Score 862.5; DB 2; Length 315;  
 Best Local Similarity 52.9%; Pred. No. 1,7e-53;  
 Matches 174; Conservative 47; Mismatches 85; Indels 23; Gaps 6;

OY 1 MRSKVALLPALLAAGAAHAEVYNRKDKLIDYKVDGLHYPSPDKDVGDDQ-TYMRL 59  
 DB 2 MKNILAVIIPALLVAGANAELIYKNGKLDYFGKMGVHWTTNGDSSDQTTARI 61  
 OY 60 GFKETOVTDLTGYGWEYQIOGNSAENENNSWTRVAFGLKFDYDGSFDPYGRN 119  
 DB 62 GLKGTETINDLTGYGWEYMDASNEGSGQTTFLAFGLKAGEYSPDYGRN 121  
 OY 120 DVTSMVDLPFEGGDTYG-SPNEMQGRNFGATYRNTDFGLVGLNFAVOYQKNGNPS 178  
 DB 122 DVEATDMLVEMGSDGMNMTDNTMTGRTNGVATYRNSDFGLVGLSFALOYQGN--- 177  
 OY 179 GEGFTSGVTNNGRDALRQNGDVGSGITVDYE-GFGIGAISSSKRTDAONTAAYIGND 237  
 DB 178 -----DHDRAIRKQNGDGFSTAATYAFANDGIALSAGYSSSSNRSDQKAD---GNGD 225  
 OY 238 RAETTYGGLKYDANNITLAAYOTYATNATRVGSLGMANKAONFEAVAYOYQDFGLRPSLA 297  
 DB 226 KAEWMATSAKADANNITLAAYVYQTYNMTPEEDNHFAKTONFEAVAYOYQDFGLRPSIG 285  
 OY 298 YLQSGKNL-----GRGYDDEDILKYVDVG 322  
 DB 286 YVOTKGDLOSRAFGSGDADLVKTYIEVG 314

RESULT 14  
 O92C71 PRELIMINARY; PRT; 315 AA.  
 AC O92C71;  
 DT 01-MAY-1999 (Tremblrel, 10, Created)  
 DT 01-MAY-1999 (Tremblrel, 10, Last sequence update)  
 DT 01-MAR-2001 (Tremblrel, 16, Last annotation update)  
 DE SIMILAR TO OMPF.  
 OS Yersinia pestis.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Yersinia.

OX NCBI\_TaxID=632;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-6/69;  
 RA Buchrieser C., Rusniok C., Couve E., Frangeul L., Billault A.,  
 RA Kunst F., Carniel E., Glaser P.;  
 RT "DNA sequence of the 102 kbases unstable region of Yersinia pestis."  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AL031866; CAA21336.1;  
 DR HSSP: P02931; IGFN.  
 DR InterPro: IPR001702;  
 DR Pfam: PF00267; Gram-ve\_porins; 1.  
 DR PRINTS: PR00182; ECOLNTEPORIN.  
 SQ SEQUENCE 315 AA; 34304 MW; D32FB91828EDA17A CRC64;

Query Match 37.5%; Score 732; DB 2; Length 315;  
 Best Local Similarity 51.5%; Pred. No. 2.8e-44;  
 Matches 158; Conservative 40; Mismatches 83; Indels 26; Gaps 9;

OY 1 MRSKVALP-----LIPALLAAGAAHAEVYNRKDKLIDYKVDGLHYPSPDKDVGDDQ 55  
 DB 1 MKNILAMALATLGIIPAL-----SSAAEIVKKGSKNKLDYFGVAKYLF--KKQSNEDAT 53  
 OY 56 YMRIGFGEQVTDLTGYGWEYQIOGNSAENEN--SWTRVAFGLKFDYDGSFDPYGR 113  
 DB 54 YVRIGFGEKTKINSQLTGFGWEYNIANNTEGSDGKRNKRLRFAGLKLADYGSFDPYGR 113  
 OY 114 NYGVYVNTSWTDLPFEGGDTY--GSDNEMQGRNFGATYRNTDFGLVGLNFAVOYQ 172  
 DB 114 NYGVYVNTSWTDLPFEGGDSMATNTYARSTGLATYRNTDFGLVGLNFAVOYQ 173  
 OY 173 KGNPSEGEFTSGVTNNGRDALRQNGDVGSGITY-DYEGFGI--GGAISSSKRTDAONT 229  
 DB 174 RNED-----GDVTRNERSTQKANGDGFGLSTFYQNIQSGVFAAAYSSSNTBEQKE 226  
 OY 230 AAYIGNDRAETTYGGLKYDANNITLAAYOTYATNATRVGSLGMANKAONFEAVAYOYD 289  
 DB 227 LVNSAAGDKAQMAYTGKLYDANNQAYIAAMYGETLNMTPYKRL-LANKQVVELVAYOYFE 285  
 OY 290 FGLRPSL 296  
 DB 286 NGIRPSL 292

## RESULT 15

O52641 PRELIMINARY; PRT; 130 AA.  
 AC O52641;  
 DT 01-NOV-1996 (Tremblrel, 01, Created)  
 DT 01-NOV-1996 (Tremblrel, 01, Last sequence update)  
 DT 01-MAR-2001 (Tremblrel, 16, Last annotation update)  
 DE OMPF (FRAGMENT).  
 GN OMPF.  
 OS Rahnelia aquatilis.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Rahnelia.  
 OX NCBI\_TaxID=34038;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CF3;  
 RA Achouak W., de Mot R., Heulin T.;  
 RL FEMS Microbiol. Ecol. 0:0-0(0).  
 DR EMBL: U17430; AAA56871.1;  
 DR HSSP: P09878; IITV.  
 DR InterPro: IPR001702;  
 DR Pfam: PF00267; Gram-ve\_porins; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 130 130  
 SQ SEQUENCE 130 AA; 14510 MW; DB6A341744A48EF5 CRC64;

Query Match 26.5%; Score 518.5; DB 2; Length 130;

Best Local Similarity 71.5%; Pred. No. 1e-29; Mismatches 18; Indels 1; Caps 1;  
 Matches 93; Conservative 18; Mismatches 18; Indels 1; Caps 1;  
 QY 23 EVYKKGDKNKLDELGKVDGLHIFSDNKNVDGDDQTYMRLGFKGETQVTDQLFTYGOMEYQIQ 82  
 Db 1 EYKKGDKNKLDELGKVDGLHIFSDNKNVDGDDQTYMRLGFKGETQVTDQLFTYGOMEYQIQ 60  
 QY 83 GNSAENEN-NSWTPVAFAPAGLKFQDVGSFQYGRNYGVVYDVTSMTPDVLPEFGDPTGSDNF 141  
 Db 61 LNTGSESDANNFTRVGFRAGLKFQGVMSLDYGRNYGVVYDVTSMTPDVLPEFGDPTGSDNF 120  
 QY 142 MOQRNFGAT 151  
 Db 121 MQRNFGAT 130

Search completed: August 21, 2001, 20:59:22  
 Job time: 97 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 21, 2001, 20:57:45 ; Search time 13.1 Seconds  
(without alignments) 959.677 Million cell updates/sec

Title: US-09-575-061-1  
Perfect score: 1953  
Sequence: 1 MRSKVALIALLPALLAAGAAH.....TRDAGINTDNIYALGLVYQF 367

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues  
Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1914	98.0	367	1 OMPC_ECOLI	P06996 escherichia
2	1539.5	78.8	378	1 OMPC_SALTI	P09878 salmonella
3	1537	78.7	363	1 OMPC_KLEPN	Q48473 klebsiella
4	1512.5	77.4	378	1 OMPC_SALTY	O52503 salmonella
5	1296	66.3	383	1 OMPC_SALTY	O56111 salmonella
6	1295	66.3	377	1 OMPC_ECOLI	P77747 escherichia
7	1283.5	65.7	376	1 OMPC_SERMA	O54471 serratia ma
8	1241	63.5	374	1 OMPC_SERMA	O33980 serratia ma
9	1220	62.5	342	1 OMPC_RAHQ	O33507 rahnelia aq
10	1213.5	62.1	394	1 OMPC_SALTI	O56110 salmonella
11	1187	60.8	397	1 YEDS_ECOLI	P76335 escherichia
12	1177	60.3	365	1 OMPC_ECOLI	P21420 escherichia
13	1169	59.9	365	1 OMPC_ECOLI	P07228 bacterioph
14	1129.5	57.8	350	1 OMPC_ECOLI	Q47480 enterobacte
15	1109	56.8	351	1 OMPC_ECOLI	P02932 escherichia
16	1104	56.5	351	1 OMPC_ECOLI	P02932 escherichia
17	1086	55.6	351	1 OMPC_ECOLI	O01605 citrobacter
18	1065.5	54.6	350	1 OMPC_SALTY	P30705 salmonella
19	1060	54.3	349	1 OMPC_SALTY	O01606 klebsiella
20	1059	54.2	351	1 OMPC_SALTY	P30704 klebsiella
21	1055.5	54.0	350	1 OMPC_SALTY	O56113 salmonella
22	1029.5	52.6	363	1 OMPC_SALTY	P37432 salmonella
23	1027.5	52.6	363	1 OMPC_SALTY	O56828 xenorhabdus
24	1002	51.3	369	1 OMPC_SALTY	P37552 salmonella
25	882	45.2	382	1 OMPC_SALTY	P57440 buchnera ap
26	592	30.3	341	1 OMPC_SALTY	O52581 photobacter
27	289	14.8	341	1 OMPC_SALTY	P97085 vibrio chol
28	279	14.3	363	1 OMPC_SALTY	O48220 haemophilus
29	196	10.0	363	1 OMPC_SALTY	O48219 haemophilus
30	194.5	10.0	371	1 OMPC_SALTY	P46027 haemophilus
31	194.5	10.0	361	1 OMPC_SALTY	O48217 haemophilus
32	192.5	9.9	361	1 OMPC_SALTY	O48217 haemophilus
33	191.5	9.8	369	1 OMPC_SALTY	O48218 haemophilus

34	189	9.7	360	1 OMPC_ECOLI	O48216 haemophilus
35	187.5	9.6	353	1 OMPC_ECOLI	O48221 haemophilus
36	176	9.0	386	1 OMPC_ECOLI	P46026 haemophilus
37	174.5	8.9	326	1 OMPC_ECOLI	P29739 photobacter
38	173.5	8.9	385	1 OMPC_ECOLI	P46025 haemophilus
39	164.5	8.4	361	1 OMPC_ECOLI	P20149 haemophilus
40	163.5	8.4	359	1 OMPC_ECOLI	P43839 haemophilus
41	154	7.9	348	1 OMPC_ECOLI	P20148 haemophilus
42	153	7.8	348	1 OMPC_ECOLI	P18195 neisseria g
43	152.5	7.8	385	1 OMPC_ECOLI	O04064 bordetella
44	141	7.2	351	1 OMPC_ECOLI	P24305 comamonas a
45	140	7.2	393	1 OMPC_ECOLI	P13415 neisseria m

## ALIGNMENTS

RESULT	ID	OMPC_ECOLI	STANDARD	PRT	367 AA
AC	P06996				
DT	01-APR-1988 (Rel. 07, Created)				
DT	01-APR-1988 (Rel. 07, Last sequence update)				
DT	01-OCT-2000 (Rel. 40, Last annotation update)				
DE	OUTER MEMBRANE PROTEIN C PRECURSOR (PORIN OMPC) (OUTER MEMBRANE PROTEIN 1B).				
GN	OMPC OR MECA OR PAR.				
OS	Escherichia coli.				
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.				
OX	NCBI_TaxID=562;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=83213433; PubMed=6304064;				
RA	Mizuno T., Chou M.-Y., Inouye M.;				
RT	"A comparative study on the genes for three porins of the Escherichia coli outer membrane. DNA sequence of the osmoregulated omp gene.";				
RJ	J. Biol. Chem. 258:6932-6940(1983).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRATIN-K12 / M6165;				
RX	MEDLINE=9742617; PubMed=9278503;				
RA	Baltner F.R., Plunkett G., Iii, Bloch C.A., Perna N.T., Burland V., Nakade S., Colldo-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;				
RT	"The complete genome sequence of Escherichia coli K-12.";				
RL	Science 277:1233-1238(1997).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=97251358; PubMed=9097040;				
RA	Itch T., Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M., Nakade S., Nakai T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N., Sempel G., Seki Y., Sivasubramanian S., Tagami H., Takada J., Takemoto K., Wada C., Yamamoto Y., Horuchi T.;				
RT	"A 460-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map.";				
RL	DNA Res. 3:379-392(1996).				
RN	[4]				
RP	SEQUENCE OF 218-367 FROM N.A.				
RC	STRATIN-K12 / BHB2600;				
RA	Richerich P., Lahey N., Gryan G., Jaehn L., Mintz L., Robison K., Church G.M.;				
RL	Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.				
RN	[5]				
RP	SEQUENCE OF 1-22 FROM N.A., AND SEQUENCE OF 22-40.				
RX	MEDLINE=8332326; PubMed=6297988;				
RA	Mizuno T., Chou M.-Y., Inouye M.;				
RT	"DNA sequence of the promoter region of the ompc gene and the amino acid sequence of the signal peptide of pro-Ompc protein of				

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RT Escherichia coli."
RL FEBS Lett. 151:159-164(1983).
RN [6]
RP SEQUENCE OF 32-57 FROM N.A.
RX MEDLINE=86033642; PubMed=2997131;
RA Nogami T., Mizuno T., Mizushima S.;
RT "Construction of a series of ompF-ompC chimeric genes by in vivo
RT homologous recombination in Escherichia coli and characterization of
RT the translational products."
RL J. Bacteriol. 164:797-801(1985).
RN [7]
RP SEQUENCE OF 22-30.
RX STRAIN=K12 / EMG2;
MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
RT in the genome of Escherichia coli K-12."
RL Electrophoresis 18:1259-1313(1997).
RN [8]
RP SEQUENCE OF 22-26.
RX STRAIN=K12 / M3110;
MEDLINE=98291876; PubMed=9629924;
RA Molloy M.P., Herbert B.R., Walsh B.J., Tyler M.I., Traini M.,
RA Sanchez J.-C., Hochstrasser D.F., Williams K.L., Gooley A.A.;
RT "Extraction of membrane proteins by differential solubilization for
RT separation using two-dimensional gel electrophoresis."
RL Electrophoresis 19:837-844(1998).
CC -1- FUNCTION: FORM PASSIVE DIFFUSION PORES WHICH ALLOW SMALL MOLECULAR
CC WEIGHT HYDROPHILIC MATERIALS ACROSS THE OUTER MEMBRANE.
CC -1- SUBUNIT: HOMOTRIMER.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
CC -1- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
CC -----
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CC -----
DR EMBL: K00541; AAA24243.1;
DR EMBL: AE000310; AAC75275.1;
DR EMBL: D90850; BAA15998.1;
DR EMBL: U00008; AAA16412.1;
DR PIR: A20867; MMECP.
DR PIR: B25029; B25028.
DR PIR: A18883; A18885.
DR HSSP: P02931; IGFN.
DR ECO2DBASE: A035.5; 6TH EDITION.
DR EcoGene: EG10670; ompC.
DR InterPro: IPR001702; -.
DR InterPro: IPR001897; -.
DR Pfam: PF00267; Gram-ve_porins; 1.
DR PRINTS: PR00182; ECOLIEMPORIN.
DR PRINTS: PR00183; ECOLIEMPORIN.
DR PROSITE: PS00576; GRAM_NEG_PORIN; 1.
KW Outer membrane; Transmembrane; Porin; Phage recognition; Signal.
FT SIGNAL 1 21
FT CHAIN 1 367
FT SEQUENCE 367 AA; 40368 MW; 6A49370CC8A1A225 CRC64;
SQ

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Query Match          98.0%; Score 1914; DB 1; Length 367;
Best Local Similarity 98.1%; Pred. No. 7.8e-126;
Matches 360; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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OY 1 MKSKVALLIPALLAAGAAHAAYNNKDKNKLDPYGVDELHFHFSNDKVDGQDTYWRIG 60
DB 1 MKKVVSLVLPALLVAGAAANAAYNNKDKNKLDPYGVDELHFHFSNDKVDGQDTYWRIG 60
OY 61 FKKEIVTDLTGTGOMWEYIOGNSAENENNSWTRVAFAGLKFQDVGSEFDYGRNYGVYD 120

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DB 61 FKKEIVTDLTGTGOMWEYIOGNSAENENNSWTRVAFAGLKFQDVGSEFDYGRNYGVYD 120
OY 121 VTSWTDVLPFEGGDTYGSNDPMOORGNFATYRTDFEGLVDGINFVVOYOGKNGNPSGE 180
DB 121 VTSWTDVLPFEGGDTYGSNDPMOORGNFATYRTDFEGLVDGINFVVOYOGKNGNPSGE 180
OY 181 GFTSGVTNNRDLRONGDVGSGITVDYEGFISGAISSSKRTDAQNTAAYTGNDRAE 240
DB 181 GFTSGVTNNRDLRONGDVGSGITVDYEGFISGAISSSKRTDAQNTAAYTGNDRAE 240
OY 241 TYTGELKYDANNIYLAQYQTINATRVGSLGWANKAQNFEAAVQYQFDFGLRPSLAYLQ 300
DB 241 TYTGELKYDANNIYLAQYQTINATRVGSLGWANKAQNFEAAVQYQFDFGLRPSLAYLQ 300
OY 301 SKGKNLGRGVDDEDIKYYVVGATFYFNKMSYVDYKINLLDNOFTRDAGINTDNIYA 360
DB 301 SKGKNLGRGVDDEDIKYYVVGATFYFNKMSYVDYKINLLDNOFTRDAGINTDNIYA 360
OY 361 LGLVYQF 367
DB 361 LGLVYQF 367

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RESULT 2
OMP_C_SALTI STANDARD; PRT; 378 AA.
ID OMP_C_SALTI
AC P09878;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE OUTER MEMBRANE PROTEIN C PRECURSOR (PORIN OMP_C).
GN OMP_C.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90060831; PubMed=2684785;
RA Puente J.L., Alvarez-Scherer V., Gosset G., Calva E.;
RT "Comparative analysis of the Salmonella typhi and Escherichia coli
RT ompC genes."
RL Gene 83:197-206(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=TY2;
MEDLINE=88319959; PubMed=3412902;
RA Venegas A., Gomez I., Zator I., Yudelevich A.;
RT "The nucleotide sequence of the Salmonella typhi ompC porin gene."
RN Nucleic Acids Res. 16:7721-7721(1988).
RN [3]
RP 3D-STRUCTURE MODELING AND CRYSTALLIZATION.
RX MEDLINE=99332091; PubMed=10405180;
RA Brocklasamy A., Krishnaswamy S.;
RT "Crystallization of the immunodominant outer membrane protein OmpC;
RT the first protein crystals from Salmonella typhi, a human pathogen."
RL FEBS Lett. 453:380-382(1999).
CC -1- FUNCTION: FORM PASSIVE DIFFUSION PORES WHICH ALLOW SMALL MOLECULAR
CC WEIGHT HYDROPHILIC MATERIALS ACROSS THE OUTER MEMBRANE.
CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
CC -1- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
CC -----
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CC -----
DR EMBL: M31424; AAA27169.1;
DR EMBL: X07835; CAA30688.1;

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DR PIR: J00119; MMEBPC.
DR PIR: S01248; S01248.
DR PDB: 1IIV; 14-OCT-98.
DR InterPro: IPR001702; -.
DR InterPro: IPR001897; -.
DR Pfam: PF00267; Gram-ve-porins; 1.
DR PRINTS: PR00182; ECOLNEIPORIN.
DR PRINTS: PR00183; ECOLIPORIN.
DR PROSITE: PS00576; GRAM_NEG_PORIN; 1.
KW Outer membrane; Transmembrane; Porin; Phage recognition; Signal;
FT SIGNAL 1 21
FT CHAIN 22 378 OUTER MEMBRANE PROTEIN C.
FT CONFLICT 362 362 MISSING (IN REF. 2).
SQ SEQUENCE 378 AA; 41239 MW; 58479E8685B43ED1 CRC64;

Query Match 78.8%; Score 1539.5; DB 1; Length 378;
Best Local Similarity 77.3%; Pred. No. 7.1e-100;
Matches 297; Conservative 24; Mismatches 40; Indels 23; Gaps 5;

DY 1 M K S V Y L A L I P A L L A A G A H A E Y N K D G N K L D Y G K V D G L H Y F S D N K D V D G D Q T Y M R L G 60
DB 1 M K V Y L S L V P A L L Y A G A N A A E I Y N K D G N K L D F G K Y D G L H Y F S D D G S D G D Q T Y M R I G 60
DY 61 F K G E Q V T D Q L T G Y G O M E Y O I Q G N S A E N N S W T R V A F A G L K F O D V S G S F D Y G R N Y G V Y D 120
DB 61 F K G E Q V N D Q L T G Y G O M E Y O I Q G N O T E G S N D S W T R V A F A G L K F D A G S F D Y G R N Y G V Y D 120
DY 121 V T S W T D V L P E F G G D T Y G S D N F M O Q R N G A T Y R N T D F F G L Y D G L N F A V O Y G K N G N S P G E 180
DB 121 V T S W T D V L P E F G G D T Y G A D N F M O Q R N G A T Y R N T D F F G L Y D G L D F A L O Y G K N G S V S G E 180
DY 181 G F T S G V T N G R D A L R O N G D V G S G S I T Y D Y - E G F G I G A I S S S K R T D A O N T A A - - - Y I N G 236
DB 181 - - - - - N T N G S L N Q N D G I G G S S I T Y A I G E G F S V G A I T T S K R T A D O N T A M A R L I N G 234
DY 237 D R A E T Y T G L K Y D A N N I Y L A A Q T Y Q T Y N A T R V G - - - - - S L G M A N K A O N F E A V A Q Y 287
DB 235 D R A T Y T G T G L K Y D A N N I Y L A A Q Y S Q T Y N A T R F G T S N G S N P S T S G F A N K A O N F E V A Q Y 294
DY 288 F D E G L R P S L A L O S K R N L G R G - - - - - Y D D E I L K Y V D Y G A T Y Y R N K N M S T Y V D K I N L D 343
DB 295 F D F G L R P S V A A L O S K R G K I S N G S G A S Y G D D I V R Y V D G A T Y Y F N K N M S T Y V D Y K I N L D 354
DY 344 D N O F T R D A G I N T D N I V A L G L Y O F 367
DB 355 K N D F T R D A G I N T D I V A L G L Y O F 378

RESULT 3
OMPC_KLEPN STANDARD; PRT; 363 AA.
AC Q48473;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE OUTER MEMBRANE PROTEIN C PRECURSOR (PORIN OMPC) (PORIN OMPK36).
GN OMPC OR OMPK36.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
OX NCBI_Taxid=573;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=C3;
RA MEDLINE=951172739; PubMed=7868262;
RA Albert S., Rodriguez-Quijones F., Schirmer T., Rummel G., Tomas J.M.,
RA Rosenbusch J.P., Benedi V.J.;
RT "A porin from Klebsiella pneumoniae: sequence homology, three-
dimensional model, and complement binding.";
RL Infect. Immun. 63:903-910(1995).
RN [2]

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RP X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS).
RX MEDLINE=99216538; PubMed=10196126;
RA Dutzler R., Rummel G., Albert S., Hernandez-Alles S., Phale P.S.,
RA Rosenbusch J.P., Benedi V.J., Schirmer T.;
RT "Crystal structure and functional characterization of OmpK36, the
RT osmoporin of Klebsiella pneumoniae.";
RL Structure 7:425-434(1999).
CC -1- FUNCTION: FORM PASSIVE DIFFUSION PORES WHICH ALLOW SMALL MOLECULAR
CC WEIGHT HYDROPHILIC MATERIALS ACROSS THE OUTER MEMBRANE. IN
CC K. PNEUMONIAE IT HAS BEEN SHOWN TO BIND C10 COMPONENT AND ACTIVATE
CC THE CLASSICAL PATHWAY OF THE COMPLEMENT SYSTEM.
CC -1- SUBUNIT: HOMOTRIMER.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
CC -1- SIMILARITY: BELONGS TO THE OMPC/PHO E FAMILY OF PORINS.
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CC -----
DR EMBL: Z33506; CA83913.1; -.
DR PDB: 1OSM; 26-JUL-99.
DR InterPro: IPR001702; -.
DR InterPro: IPR001897; -.
DR Pfam: PF00267; Gram-ve-porins; 1.
DR PRINTS: PR00182; ECOLNEIPORIN.
DR PRINTS: PR00183; ECOLIPORIN.
DR PROSITE: PS00576; GRAM_NEG_PORIN; 1.
KW Outer membrane; Transmembrane; Porin; Signal; 3D-structure.
FT SIGNAL 1 21
FT CHAIN 22 363 OUTER MEMBRANE PROTEIN C.
SQ SEQUENCE 363 AA; 39663 MW; 9DE45546F01F116C CRC64;

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Query Match 78.7%; Score 1537; DB 1; Length 363;
Best Local Similarity 78.9%; Pred. No. 1e-99;
Matches 291; Conservative 32; Mismatches 38; Indels 8; Gaps 5;

DY 1 M K S V Y L A L I P A L L A A G A H A E Y N K D G N K L D Y G K V D G L H Y F S D N K D V D G D Q T Y M R L G 60
DB 1 M K V Y L S L V P A L L Y A G A N A A E I Y N K D G N K L D I G K I D G L H Y F S D D G S D G D Q T Y M R I G 60
DY 61 F K G E Q V T D Q L T G Y G O M E Y O I Q G N S A E N N S W T R V A F A G L K F O D V S G S F D Y G R N Y G V Y 119
DB 61 V K G E Q I N D Q L T G Y G O M E Y N V O A N T E S S D O A W T R L F A G L K F D A G S F D Y G R N Y G V Y 120
DY 120 D V T S W T D V L P E F G G D T Y G S D N F M O Q R N G A T Y R N T D F F G L Y D G L N F A V O Y G K N G N P S G 179
DB 121 D V T S W T D V L P E F G G D T Y G S D N F L O S R A N G V A T Y R S D F G L Y D G L N F A L O Y G K N G S V S G 180
DY 180 E G F T S G V T N G R D A L R O N G D V G S G I T Y D - Y E G F G I G A I S S S K R T D A O N T A A I Y G N D R 238
DB 181 E - - - - - G A T N N G R G A L K O N G D F G T S V T D I D G I S A G F A V A N S K R T D O N - Q L L G E G D H 235
DY 239 A E T Y T G L K Y D A N N I Y L A A Q T Y Q T Y N A T R V S L G A N K A O N F E A V A Q Y O F D F G L R P S V A Y 298
DB 236 A E T Y T G L K Y D A N N I Y L A Q T Y Q T Y N A T R A G S L G F A N K A O N F E A V A Q Y O F D F G L R P S V A Y 295
DY 299 L O S K R N L G R G Y D D E I L K Y V D Y G A T Y Y F N K N M S T Y V D Y K I N L D N O F T R D A G I N T D N I 358
DB 296 L O S K G K D L - N G Y G D D I L K Y V D G A T Y Y F N K N M S T Y V D Y K I N L D N S F T S A G I S T D V 354
DY 359 V A L G L Y O F 367
DB 355 V A L G L Y O F 363

RESULT 4
OMPC_SALTY STANDARD; PRT; 378 AA.
ID OMPC_SALTY

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AC 052503;3998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE OUTER MEMBRANE PROTEIN C PRECURSOR (PORIN OMPc).
GN OMPc.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae.
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=ATCC 14028;
RL Negm R.S., pistole T.G.;
CC submitted (Dec-1997) to the EMBL/GenBank/DBJ databases.
CC -I FUNCTION: FORM PASSIVE DIFFUSION PORES WHICH ALLOW SMALL MOLECULAR
CC WEIGHT HYDROPHILIC MATERIALS ACROSS THE OUTER MEMBRANE.
CC -I SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -I SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
CC -I SIMILARITY: BELONGS TO THE OMPc/PHO FAMILY OF PORINS.
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CC -----
DR EMBL: AF039309; AAB96675.1; -
DR StyGene; SG10675; ompc.
DR InterPro; IPR001702; -.
DR InterPro; IPR001897; -.
DR Pfam; PF00267; Gram-ve_porins; 1.
DR PRINTS; PR00182; ECOLIPEPORIN.
DR PRINTS; PR00183; ECOLIPEPORIN.
DR PROSITE; PS00576; GRAM_NEG_PORIN; 1.
DR Outer membrane; Transmembrane; Porin; Phage recognition; Signal.
KM SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 378 OUTER MEMBRANE PROTEIN C.
SQ SEQUENCE 378 AA; 41299 MW; FC294209A91D79FA CRC64;

Query Match 77.4%; Score 1512.5; DB 1; Length 378;
Best Local Similarity 76.6%; Pred. 5.2e-98;
Matches 294; Conservative 26; Mismatches 41; Indels 23; Gaps 6;

QY 1 MSKYIALILIPLLAAGAAAEVYNNKGNKRLDYLGVKVDGLHPSDNKDVSODPQYMBLG 60
DB 1 MKYKVLISLVLPALVAGANAIAEYNNKGNKRLDYLGVKVDGLWTFSDDDGSDSDQYMRIG 60
QY 61 FKGQTVTDQLTGYGQWEXYIOGNSAENENNSWTVAAAGLKFQDVGSEFDYGRNRYVD 120
DB 61 FKGQTVTDQLTGYGQWEXYIOGNSAENENNSWTVAAAGLKFQDVGSEFDYGRNRYVD 120
QY 121 VTSWTDVLPPEFGDPTGYSDFNFMQGRNFGATYRNTDFGLVDGLNFAVQYOGKNSPGE 180
DB 121 VTSWTDVLPPEFGDPTGYSDFNFMQGRNFGATYRNTDFGLVDGLNFAVQYOGKNSPGE 180
QY 181 GFTSGVTNNGRALQNGDVGSGSTTYD -EFGIGGAISSSKRT-DQONT--AAYING 236
DB 181 -----NTNGRSLNQNGDVGSGSLTYAIGEGFVSVAITTSKRPADDDNANAALYNG 234
QY 237 DEAEYTYGGLKTDANNITYLAQYTYTVNATRG-----SLGMAKQNFEEVAAYQ 287
DB 237 DEAEYTYGGLKTDANNITYLAQYTYTVNATRG-----SLGMAKQNFEEVAAYQ 287
QY 294 DRAIYTYTGGGLKTDANNITYLAQYFOTYNAATRGTSNGSNPSTSYGFANKAONFEVVAQY 294
DB 294 DRAIYTYTGGGLKTDANNITYLAQYFOTYNAATRGTSNGSNPSTSYGFANKAONFEVVAQY 294
QY 343 FDEGLRPSLAYLQSGKGNLGRG---YDDEDILKVVYDVGATYFENKNSYVDYKTNLND 343
DB 343 FDEGLRPSLAYLQSGKGNLGRG---YDDEDILKVVYDVGATYFENKNSYVDYKTNLND 343
QY 367 DNGQTRDAGINTDNIVALGLVYQF 367
DB 367 DNGQTRDAGINTDNIVALGLVYQF 367

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Db      355  KYEFTRDAGINDDVALGLVYQF 378

RESULT      5
ID           OMS2_SALTI      STANDARD:      PRT:      383 AA.
AC           05611:
DT      15-DEC-1998 (Rel. 37, Created)
DT      15-DEC-1998 (Rel. 37, Last sequence update)
DT      15-DEC-1998 (Rel. 37, Last annotation update)
DE      OUTER MEMBRANE PROTEIN S2 PRECURSOR.
GN      OMP52.
OS      Salmonella typhi.
OC      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC      Salmonella.
OX      NCBI.TaxID=601;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=IMSS-1;
RA      Fernandez-Mora M., Calva E.;
RL      Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
CC      -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE
CC      (BY SIMILARITY)
CC      -1- SIMILARITY: BELONGS TO THE OMP/C/PHO FAMILY OF PORINS.
CC      -----
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CC      entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC      or send an email to license@sib-sib.ch).
CC      -----
DR      EMBL: X89756; CAA61903.1; -
DR      InterPro: IPR001702; -
DR      InterPro: IPR001897; -
DR      Pfam: PF00267; Gram-ve_porins; 1.
DR      PRINTS: PR00182; ECOLIPEPORIN.
DR      PRINTS: PR00183; ECOLIPEPORIN.
KW      Outer membrane; Transmembrane; Porin; Signal.
FT      SIGNAL      1      21      POTENTIAL.
FT      CHAIN      22      383      OUTER MEMBRANE PROTEIN S2.
SQ      SEQUENCE      383 AA; 42183 MW; 47CFB6B5F6A2370F CRC64;

Query Match      66.4%; Score 1296; DB 1; Length 383;
Best Local Similarity      66.8%; Pred. No. 5.3e-83;
Matches      256; Conservative      37; Mismatches      74; Indels      16; Gaps      8;

OY      1      M K S V L A L L I P A L L A A G A A H A E Y N N K D G N K L D L G K V D G L H F S D N K D V D G D Q T Y M R I G      60
DB      1      M K R R V A L V I P A L L A A G A A H A E I Y N K D G N K L D L G K V D G L H F S D S S K D D Q Y M R I G      60
OY      61      F K G E F V T D Q L T G Y G O M E Y O I D G N S A E N D N - N S K T R V A F A G I K F D V S S P D Y G R N Y G V Y      119
DB      61      F K G E I O I N D O L T G Y G O W E Y N V O A N T T E E G A N S W T R L A F A G I K F E D Y S F P Y G R N Y G V L Y      120
OY      120      D Y T S T D V L P E R G C G T Y G - S D N F M O R G N F G T Y N T P F G L Y V D L N A V O Y O G N G N P S      178
DB      121      D V E G M T D M L P E R G G S Y T A D Y A D Y M T G R A N G V A Y T N T D P F G L Y V D L N L R L O T O G R N E S O S      180
OY      179      G E G F S G T V - - N G R D A L R O N G D G V G S I T Y D Y - E G F I G G A I S S S K R T D A Q - N T A A Y I G      234
DB      181      A D D V A I G I N N R N N G D I Y N D G D G S I T T Y D I G M F S A G A A Y T T S D R T N E Q V A N G I T A      240
OY      235      N G D R A E I Y T G G I K Y D A N N I Y L A A O Y T O T Y N A T R V G S L - - - - - G M A K A Q N F E A V A O Y Q F      288
DB      241      G G D K A D A M T A G I K Y D A N N I Y L A T M S E I R N M T P Y K T D K G Y D G V A A N T O N F E V A Y A O Y Q F      300
OY      289      D E G L R P A S I A Y O S K G K N L - - - G R G V D E D D I L K Y V D G A F Y F E N K M S Y Y V D Y K I N L L D N      345
DB      301      D F G L R P A V S F L M S K G K D L T Y N N N G D D D L V N K I A V G A Y T F E N K M S Y Y V D I K I N L L D D D      360

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OY 346 Q-FTRDAGINTDNIYALGVYQF 367  
 DB 361 DPEYKADGISTDIDVALGVYQF 383

# RESULT 6

OMP\_N\_ECOLI  
 ID OMPN\_ECOLI STANDARD; PRT; 377 AA.  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE OUTER MEMBRANE PROTEIN N PRECURSOR (PORIN OMEN).  
 GN OMPN.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia  
 NC NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12 / MG1655;  
 RX MEDLINE-97426617; PubMed-9278503;  
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12.";  
 RL Science 277:1453-1474(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12;  
 RX MEDLINE-97251357; PubMed-9097039;  
 RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,  
 RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,  
 RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,  
 RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,  
 RA Sasaki G., Seki Y., Sivasubraman S., Tagami H., Takeda J.,  
 RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;  
 RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome  
 corresponding to the 28.0-40.1 min region on the linkage map.";  
 RL DNA Res. 3:363-377(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A., SEQUENCE OF 22-33, AND CHARACTERIZATION.  
 RX MEDLINE-98317278; PubMed-9642192;  
 RA Prilipov A., Phale P.S., Koehnlik R., Widmer C., Rosenbusch J.P.;  
 RT "Identification and characterization of two quiescent porin genes,  
 ompC and ompN, in Escherichia coli BE.";  
 RL J. Bacteriol. 180:3388-3392(1998).  
 CC -1- FUNCTION: NON-SPECIFIC PORIN.  
 CC -1- SUBUNIT: HOMOMER.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, OUTER MEMBRANE.  
 CC -1- SIMILARITY: BELONGS TO THE OMP/PHO FAMILY OF PORINS.  
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 CC -----  
 CC EMBL: AE000234; AAC74459.1; -  
 CC EMBL: D90775; BAA14981.1; -  
 CC EMBL: D90776; BAA14986.1; -  
 CC EcoGene: EG13375; ompN.  
 CC InterPro: IPR001702; -  
 CC InterPro: IPR001897; -  
 CC Pfam: PF00267; Gram-ve\_porins; 1.  
 CC PRINTS: PR00182; ECOLNIPORIN.  
 CC PRINTS: PR00183; ECOLIPORIN.  
 CC Outer membrane; Transmembrane; Porin; Signal.  
 FT SIGNAL 1 21

FT CHAIN 22 377 OUTER MEMBRANE PROTEIN N.  
 SQ SEQUENCE 377 AA; 41220 MW; 4420D2CB9BC10F95 CRC64;

Query Match 66.3%; Score 1295; DB 1; Length 377;  
 Best Local Similarity 67.8%; Pred. No. 6, 1e-83;  
 Matches 261; Conservative 37; Mismatches 61; Indels 26; Gaps 10;

OY 1 MKSKVIALILPALLAAGAAHAAEYVYNDGKLDLYGVDSGLHFSPDKDVGQDTYWRIG 60  
 DB 1 MKSKVIALILPALLAAGAAHAAEYVYNDGKLDLYGVDSGLHFSPDKDVGQDTYWRIG 60  
 OY 61 FKGETOVDTLTGYGOWEYIOGNSAE-NENNSWTRVAFAGLFQDVSFDRYGVY 119  
 DB 61 FKGETOINDLTGYGOWEYIOGNSAE-NENNSWTRVAFAGLFQDVSFDRYGVY 120  
 OY 120 DVTSWTDVLPFGGDRY-GSDNEMQGRNGAVRYRNTDFGLVDGTFEAYOYQKGNPS 178  
 DB 121 DIEGWTDMLPEFGSDTYNADNMTGRANGVATYRNTDFGLVNGLNFAVOYQGN- 176  
 OY 179 GEGFTSGV--TNGRDALRONGDVGSGITYDY-EGFGIGSAISSKRTDAQ--NTPAYI 233  
 DB 177 -EGASNGQEGSTNNGRQVREHNGDGMGLSTYDGLMGFSAGAATSSDRINDYVHTAA- 233  
 OY 234 GNCDRAEYTYGLKYDANNITYLAQTYQYNAFVSGW--ANKAQNFEAVAYQDFG 291  
 DB 234 -GGDKADAWTAGLKVDANNITYLATWYSETRNMTPEFGSDVAVANKQNEFVTAQYQDFG 292  
 OY 292 LRPSLAVYLOSKGNL-----GRGYDEDILKYDVGYATYFNKMSYVYDKINLID 343  
 DB 293 LRPAVSFLMSKGRDLHAAGADNPAGVDKLVKADYDAGTYTFNNMSTYVYDKINLID 352  
 OY 344 -DNQFTRDAGINTDNIYALGVYQF 367  
 DB 353 EDDSFYANGISTDIDVALGVYQF 377  
 RESULT 7  
 OMP\_C\_SERMA  
 ID OMP\_C\_SERMA STANDARD; PRT; 376 AA.  
 AC 054471;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DE OUTER MEMBRANE PROTEIN C PRECURSOR (PORIN OMC).  
 GN OMC.  
 OS Serratia marcescens.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Serratia.  
 NC NCBI\_TaxID=615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-UOC-51;  
 RX MEDLINE-94236242; PubMed-8190703;  
 RA Hutsul J.A.M., Worobec E.A.;  
 RT "Molecular characterization of a 40 kDa OmpC-like porin from Serratia  
 marcescens.";  
 RL Microbiology 140:379-387(1994).  
 CC -1- FUNCTION: FORM PASSIVE DIFFUSION PORES WHICH ALLOW SMALL MOLECULAR  
 CC WEIGHT HYDROPHILIC MATERIALS ACROSS THE OUTER MEMBRANE.  
 CC -1- SUBUNIT: HOMOMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, OUTER MEMBRANE.  
 CC -1- SIMILARITY: BELONGS TO THE OMP/PHO FAMILY OF PORINS.  
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 CC -----  
 CC EMBL: L24960; AAA26562.1; -

DR InterPro: IPR001702; -  
 DR InterPro: IPR001897; -  
 DR Pfam: PF00267; Gram-ve.porins; 1.  
 DR PRINTS: PRO0182; ECOLNEIPORIN.  
 DR PRINTS: PRO0183; ECOLIPORIN.  
 DR PROSITE: PS00576; GRAM\_NEG\_PORIN; 1.  
 DR Outer membrane; Transmembrane; Porin; Phage recognition; Signal.  
 FT SIGNAL 1 21 BY SIMILARITY.  
 FT CHAIN 1 22 OUTER MEMBRANE PROTEIN C.  
 FT SEQUENCE 376 AA: 41440 MW: 81227FE8515B568E CRC64;

Query Match 65.7%; Score 1283.5; DB 1; Length 376;  
 Best Local Similarity 65.6%; Pred. No. 3.8e-82;  
 Matches 252; Conservative 48; Mismatches 59; Indels 25; Gaps 8;

QY 1 MKSKVALLPALLAAGAAHAAYVYKDKGKLDLYGKVDGLHFSDNKDYDGQTYMRIG 60  
 DB 1 MKLRVLSLWPAALLVAGTAGAAEITVYKDKGKLDLYGKVDGLHFSNNNGVDGDSYMRFG 60  
 QY 61 FKGETVTDLTGYGMEYOIOGNSAENENN-SWTRVAFAGLFPDVGSPDYGRNYGVY 119  
 DB 61 LRGETVTDLTGYGMEYVIANLHAENQDNKFTKRGFAGLFGDYGSFDYGRNTGVLY 120  
 QY 120 DVTSWTDVLPFEGGDTYGSDFNFMQORNGFATYRNTDFGLVDGLNFAVOYOGKNGNP 179  
 DB 121 DVAAVTDLPFEGGDTYGAQDFMFORSSGLATYRNDFGLVDGLNFAVOYOGKNGN-G 178  
 QY 180 EGTSTVYNNRGALRONGGVGSGTIDYEGFGI--GGAISSKRTDAONTA----AT 233  
 DB 179 E-----ETNNGRVLTQNGEGYGSMSYDM-GYISAGAFAFNSRRTSEONGANGHONTM 232  
 QY 234 GNDRAETVYGLKYDANNIYLAAYTOTYNTATRVGS-----LGMANKAONFEAVAYOF 288  
 DB 233 GRDDKAEIGVSGGLKYDANDVYLAVMETQSNARFGSSDSVYGYAKKASFEAYHYOF 292  
 QY 289 DFLRLSLAYLQSGKKNLGRG---YDDEDLKYVDGATYVYFNKMSYVDYKINLTD 343  
 DB 293 DFLRLFVGVYNTKKGDLGRAGNGKDYGDQDLVKFVDLGYFEFFNKMSTYVDYKINLVD 352  
 QY 344 DNOFTRDAGINTDNIYALGLYOF 367  
 DB 353 NNDFTDAGINTDNIYVAVGLYOF 376

RESULT 8  
 OMPF\_SERMA  
 ID OMPF\_SERMA STANDARD: PRT: 374 AA.  
 AC 033980;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE OUTER MEMBRANE PROTEIN F PRECURSOR (PORIN OMPF).  
 GN OMPF.  
 OS Serratia marcescens.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Serratia.  
 OX NCBI\_TaxID=615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=OOC-51;  
 RX MEDLINE=97419518; PubMed=9274033;  
 RA Hutul J.A.M., Morobec E.A.;  
 RT "Molecular characterization of the Serratia marcescens OmpF porin,  
 and analysis of S. marcescens OmpF and OmpC osmoregulation.";  
 RL Microbiology 143:2797-2806(1997).  
 CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.  
 CC -1- SIMILARITY: BELONGS TO THE OMPF/PHOE FAMILY OF PORINS.  
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CC EMBL: U01967; AAB69103.1; ALT\_INIT.  
 DR InterPro: IPR001702; -  
 DR InterPro: IPR001897; -  
 DR Pfam: PF00267; Gram-ve.porins; 1.  
 DR PRINTS: PRO0182; ECOLNEIPORIN.  
 DR PRINTS: PRO0183; ECOLIPORIN.  
 DR PROSITE: PS00576; GRAM\_NEG\_PORIN; 1.  
 DR Outer membrane; Transmembrane; Porin; Signal.  
 FT SIGNAL 1 21 POTENTIAL.  
 FT CHAIN 1 22 OUTER MEMBRANE PROTEIN F.  
 FT SEQUENCE 374 AA: 41184 MW: BF821D385E441049 CRC64;

Query Match 63.5%; Score 1241; DB 1; Length 374;  
 Best Local Similarity 64.3%; Pred. No. 3.3e-79;  
 Matches 249; Conservative 36; Mismatches 68; Indels 34; Gaps 8;

QY 1 MKSKVALLPALLAAGAAHAAYVYKDKGKLDLYGKVDGLHFSDNKDYDGQTYMRIG 60  
 DB 2 MKRNIILAVYIPALLAAGAAHAAYVYKDKGKLDLYGKVDGLHFSKDKNDGDTYVRF 61  
 QY 61 FKGETVTDLTGYGMEYOIOGNSAENE--NNSWTRVAFAGLFPDVGSPDYGRNYGVY 118  
 DB 62 FKGETVTDLTGYGMEYVQSNHAESQGTCTKRLRFAGLKFDYDSFDYGRNTGVLY 121  
 QY 119 YDTSWTDVLPFEGGDTYGSDFNFMQORNGFATYRNTDFGLVDGLNFAVOYOGKNGNP 177  
 DB 122 YDVGWTDVLPFEGGDTYGSDFNFMQORNGFATYRNTDFGLVDGLNFAVOYOGKNGN-- 178  
 QY 178 SGEGFTSVYNNRGALRONGGVGSGTIDY-EGFGIGALISSKRTDAONTAATYICNG 236  
 DB 179 -----QNDGRDYKKNQDGMGWSISSTYDIEGVSPGAAVAASNRDOKLRSN-ERG 228  
 QY 237 DRAETVYGLKYDANNIYLAAYTOTYNTATRVGS-----LGMANKAONFEAV 283  
 DB 229 DKRADNTVGAKKYDANNIYLAAYTAETRNMTFPGGGFTYTCATENGCGFASTQNF 288  
 QY 284 AOYQDFGLRPSLAYLQSGKKNL--GRGYDDEDLKYVDGATYVYFNKMSYVDYKIN 340  
 DB 289 AOYQDFGLRPSLAYLQSGKKNLNPVG-SDQDLKYVSVGYTYVFNKMSYVDYKIN 347  
 QY 341 LDDNFTRDAGINTDNIYALGLYOF 367  
 DB 348 LDDNFTRDAGINTDNIYVAVGLYOF 374

RESULT 9  
 OMPF\_RAHAO  
 ID OMPF\_RAHAO STANDARD: PRT: 342 AA.  
 AC 033507;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE OUTER MEMBRANE PROTEIN C (PORIN OMPF) (FRAGMENT).  
 GN OMPF.  
 OS Rahmella aquatilis.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Rahmella.  
 OX NCBI\_TaxID=34038;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CF3;  
 RX MEDLINE=98132388; PubMed=9473046;  
 RA Achouak W., Pages J.M., de Mot R., Molle G., Heulin T.;  
 RT "A major outer membrane protein of Rahmella aquatilis functions as a  
 RT porin and root adhesin.";  
 RL J. Bacteriol. 180:909-913(1998).  
 CC -1- FUNCTION: FORM PASSIVE DIFFUSION PORES WHICH ALLOW SMALL MOLECULAR

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CC WEIGHT HYDROPHILIC MATERIALS ACROSS THE OUTER MEMBRANE.
CC IN R.AQUATILIS OMPC IS INVOLVED IN THE ADHESION TO WHEAT ROOTS.
CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
CC -1- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
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CC -----
CC EMBL: AJ002879; CA05726.1; -.
CC InterPro: IPR001702; -.
CC Pfam: PF00267; Gram-ve.porins; 1.
CC Outer membrane; Transmembrane; Porin.
CC NON_TER 1 342 342
CC SEQUENCE 342 AA; 37674 MW; 5B60D8FA5AD977A5 CRC64;

Query Match 62.5%; Score 1220; DB 1; Length 342;
Best Local Similarity 67.5%; Pred. No. 8.5e-78;
Matches 237; Conservative 43; Mismatches 51; Indels 20; Gaps 7;

OY 23 EYVKKDGNKLDYGVKLVGKVFYFSDNKNVDGDDQYTMRLGFGFQYVTOQLYGGOMEYQIQ 82
DB 1 EYVKKDGNKLDYGVKLVGKLVGKVFYFSDNKNVDGDDQYTMRLGFGFQYVTOQLYGGOMEYQIQ 82
OY 83 GNSAENEN-NSWTRVAFAGLKFQDVGSFQYGRNVGVYDVTSMVDVPEFGDYGSDNF 141
DB 61 LNTAESDANNFTRVAGLKFQDVGSFQYGRNVGVYDVTSMVDVPEFGDYGSDNF 120
OY 142 MOQRNGFATRYRTDFGLVDGLFAVOYOGKNGNSGEGFTSGVTNNGDALRQNGDV 201
DB 121 MFOGRNGFATRYRTDFGLVDGLFAVOYOGKNGNSGEGFTSGVTNNGDALRQNGDV 173
OY 202 GGSFTYDY-EGFGIGAISSSKRTDAQN--TAAYIGNGRRAETVYGLYDANNIYLLA 257
DB 174 GMSLTLYLGEFSAAGMMASTRSEONGRONPAITIGNBRAEYTYGGLYXANNIYLLA 233
OY 258 QYTOTYATRVG-----SLGMANKAONFEAVAYOYDFGLRPSLAYLOSKGNLGRGYD 311
DB 234 VFTQTYNA-RIGVSSDSHGYADNAQNEFAVAYOYDFGLRPSLAYLOSKGNLGRGYD 291
OY 312 DEDLTKYVDGATYFENKMSYVDYKINLDDNOFTRDAGINTDNIYALG 362
DB 292 NQNLTKYVDGATYFENKMSYVDYKINLDDNOFTRDAGINTDNIYALG 342

RESULT 10
OMSL_SALT1 STANDARD; PRT; 394 AA.
AC Q56110;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE OUTER MEMBRANE PROTEIN S1 PRECURSOR.
GN OMP_S1.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=601;
RP SEQUENCE FROM N.A.
RC STRAIN=IMSS-1;
RX MEDLINE=95309727; PubMed=7789812;
RA Fernandez-Mora M., Oropeza R., Puente J.L., Calva E.;
RT "Isolation and characterization of omsl, a novel Salmonella typhi
RL outer membrane protein-encoding gene.";
Gene 158:67-72(1995).

```

```

CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE
CC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X73237; CAAS1710.1; -.
CC InterPro: IPR001702; -.
CC Pfam: PF00267; Gram-ve.porins; 1.
CC PRINTS: PR00182; ECOLNIPORIN.
CC PROSITE: PS00576; GRAM_NEG_PORIN; 1.
CC SIGNAL: Outer membrane; Transmembrane; Porin.
CC CHAIN 1 21
CC SIGNAL 1 21
CC SEQUENCE 394 AA; 43253 MW; E7C8FEED424931D1 CRC64;

Query Match 62.1%; Score 1213.5; DB 1; Length 394;
Best Local Similarity 62.8%; Pred. No. 2.8e-77;
Matches 248; Conservative 38; Mismatches 80; Indels 29; Gaps 10;

OY 1 MRSKVALLIPALLAGAAHAAEYVKNKLDYGVKDLVLFSDNKNVDGDDQYTMRLG 60
DB 1 MNRKVALLIPALLAGAAHAAEYVKNKLDYGVKDLVLFSDNKNVDGDDQYTMRLG 60
OY 61 FKGETVDTQDLTGQGEYVIOGNSAENEN-NSWTRVAFAGLKFQDVGSFQYGRNVGVY 119
DB 61 FKGETVDTQDLTGQGEYVIOGNSAENEN-NSWTRVAFAGLKFQDVGSFQYGRNVGVY 120
OY 120 DVTSMVDVPEFGDYGRTY-GSDNFMOQRNGFATRYRTDFGLVDGLFAVOYOGKNGNS 178
DB 121 DIAMTDALPEFGDYGRTYRTDVTYMLGRTNGVATRYRTDFGLVDGLFAVOYOGKNGNS 179
OY 179 GEGFTSGVTNNG-RDALRQNGDVGSGIYDY-EGFGIGAISSSKRTDAQNTRYA---- 232
DB 180 GAGAGEGTGNGKRLARENGDFGMSYSTYDFGLSLGAAYSSSDRSDNQVARGYDGM 239
OY 233 -----IGNGRRAETVYGLYDANNIYLLAQTOTYATRV-----GSLGMANKAONFE 281
DB 240 NERNVYAGGETAERAWTGAKYDAYNYLLAMVATETRMVYGGNGEGNSIAKNTQNE 299
OY 282 AVAYOYDFGLRPSLAYLOSKGNL-----RG-----YDDEDLTKYVDGATYFENKMS 333
DB 300 VVAOYDFGLRPSLAYLOSKGNLGGQEVHRCNMKRTDLDYKYVDGATYFENKMS 359
OY 334 YVDYKINLDD-NOFTRDAGINTDNIYALGLVYQF 367
DB 360 YVDYKINLDDDEDFYANNNGIARDIYGLVYQF 394

RESULT 11
YEDS_ECOLI STANDARD; PRT; 397 AA.
AC P76335; O07986; P76336; P94747; P94748;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE POTENTIAL OUTER MEMBRANE PROTEIN YEDS PRECURSOR.
GN YEDS OR B1964/B1965/B1966.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]

```







RT Escherichia coli K-12 and phage 82.1;  
 RL J. Mol. Biol. 257:561-573(1996).  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, OUTER MEMBRANE.  
 CC MISCELLANEOUS: IN WILD-TYPE STRAINS OF E. COLI K12, THE NMPC OPEN  
 CC READING FRAME IS INTERRUPTED BY AN ISS INSERTION AND GENERATES A  
 CC HYBRID OPEN READING FRAME THAT IS NOT EXPRESSED. HOWEVER, IN  
 CC MUTANT STRAIN CS348, THE ISS ELEMENT HAS BEEN DELETED AND NMPC IS  
 CC EXPRESSED.  
 CC -1- SIMILARITY: BELONGS TO THE OMP/PHOE FAMILY OF PORINS.  
 CC -----  
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 CC -----  
 DR EMBL; M13457; AAA23728.1; ALT\_SEQ.  
 DR EMBL; AE000160; AAC73654.1; ALT\_SEQ.  
 DR EMBL; U82598; ABA0749.1; ALT\_SEQ.  
 DR EMBL; Z35442; CAA84594.1; -.  
 DR EMBL; X22587; CAA63323.1; -.  
 DR PIR; A25647; MMECNC.  
 DR HSSP; P02931; IGFN.  
 DR Ecocyc; EGI0659; nmPC.  
 DR InterPro; IPR001702; -.  
 DR InterPro; IPR001897; -.  
 DR Pfam; PF00267; Gram-ve\_porins; 1.  
 DR PRINTS; PR00182; ECOLNEIPORIN.  
 DR PRINTS; PR00183; ECOLIPORIN.  
 DR PROSITE; PS00576; GRAM\_NEG\_PORIN; 1.  
 KW Outer membrane; Transmembrane; Porin; Signal.  
 FT SIGNAL 1 23  
 FT CHAIN 24 365 OUTER MEMBRANE PORIN PROTEIN NMPC.  
 FT CONFLICT 326 326 K -> N (IN REF. 2 AND 3).  
 SQ SEQUENCE 365 AA; 40316 MW; 6E5128D4847FB4F8 CRC64;

Query Match 60.3%; Score 1177; DB 1; Length 365;  
 Best Local Similarity 62.1%; Pred. No. 8.7e-75;  
 Matches 234; Conservative 41; Mismatches 80; Indels 22; Gaps 6;

QY 1 MRSKVLAL--LIPALLAAGAAHAEEYNNKDKNLDLYGKVDGLHYFSNDKNDVGDQTYMR 58  
 DB 1 MKKLITVAISVAASVLAAMSAQAALYNNKDSNKLIDLKGNNAHFFSSNDADDDGDTTYAR 60  
 QY 59 LGFKGETOYTDLTGFGQWEYIOGNSAENENNS--WTRVAFAGLKFQDYGSPDYGRNNG 116  
 DB 61 LGFKGETOINDLTGFGQWEYEFKGNRAESQSSKDKTRLAFAGLKEGDSIDYGRNG 120  
 QY 117 VYVDVTSMTDVLPEFGGDY--GSDNFMQORGNFGATYRTNDFGLVDGLNFAVOYGRKNG 175  
 DB 121 VAYDIGAMTDVLPDEFQDWTQTQDVMTQRTATVATYRNNDPFGLDGLNFAAOYGRKND 180  
 QY 176 NPSGEGFTSGVTNNGDALRONGDVGSGSTTYDEGFGIGALSSSKRRDAONTAAYT-- 233  
 DB 181 RSPDNTWTE-----KDGFGFSATYTYEGFGIGATYAKAKSDRDTDTQVNAAGVLP 229  
 QY 234 ---GNGDRAETTYGGLKYDANNITVLAAYTQTYNATRVGSLGNKNAQNEAVALQYQDFE 290  
 DB 230 EYVASGKNAEVMMAAGLKYDANNITVLAATYSETQNTVFADHFAVANKAQNFEAVALQYQDFE 289  
 QY 291 LGFKGETOYTDLTGFGQWEYIOGNSAENENNS--WTRVAFAGLKFQDYGSPDYGRNNG 116  
 DB 290 GLRPSVAILOSCKRDLG--WGDODLVKYYDVAGATYFKKNNSTFVDYKINLIDKNDFTKA 348  
 QY 351 AGINTDNIVALLGLVYOF 367  
 DB 349 LGVSTDIVAVGLVYOF 365

RESULT 13

PORL\_BPPA2  
 ID PORL\_BPPA2 STANDARD; PRT; 365 AA.  
 AC P07238;  
 DT 01-APR-1988 (Rel. 07, Created)  
 DT 01-APR-1988 (Rel. 07, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE OUTER MEMBRANE PORIN PROTEIN LC PRECURSOR.  
 GN LC.  
 OS Bacteriophage PA-2.  
 OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae.  
 OX NCBI\_TaxId=10738;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86304457; PubMed=3017988;  
 RA Blahand A.J., Marcotte W.R. Jr., Schaitman C.A.;  
 RT "Structure of the lc and nmPC outer membrane porin protein genes of  
 RT lambdaoid bacteriophage".  
 RL J. Biol. Chem. 261:12723-12732(1986).  
 CC -1- FUNCTION: PORINS ARE MAJOR PROTEINS FOUND IN THE OUTER MEMBRANES  
 CC OF GRAM-NEGATIVE BACTERIA WHERE THEY FORM CHANNELS FOR THE  
 CC NONSPECIFIC PERMEATION OF SMALL SOLUTES (MOLECULES WITH MW LOWER  
 CC THAN 4000-6000 DALTONS).  
 CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, OUTER MEMBRANE  
 CC (BY SIMILARITY).  
 CC -1- MISCELLANEOUS: A PORIN GENE CAN ALSO BE FOUND IN THE GENOMES OF  
 CC CERTAIN LAMBDOID BACTERIOPHAGE, AND ITS PROTEIN IS EXPRESSED IN  
 CC THE LYSGENIC STATE. IN E. COLI THE EXPRESSION OF OMP AND OMPF  
 CC PROTEINS IS THEN REDUCED SUBSTANTIALLY.  
 CC -1- SIMILARITY: BELONGS TO THE OMP/PHOE FAMILY OF PORINS.  
 CC -----  
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 CC -----  
 DR EMBL; J02580; AAA2301.1; -.  
 DR PIR; D25647; MMBP2.  
 DR HSSP; P02931; IGFN.  
 DR InterPro; IPR001702; -.  
 DR InterPro; IPR001897; -.  
 DR Pfam; PF00267; Gram-ve\_porins; 1.  
 DR PRINTS; PR00182; ECOLNEIPORIN.  
 DR PRINTS; PR00183; ECOLIPORIN.  
 DR PROSITE; PS00576; GRAM\_NEG\_PORIN; 1.  
 KW Outer membrane; Transmembrane; Porin; Signal.  
 FT SIGNAL 1 23  
 FT CHAIN 24 365 OUTER MEMBRANE PORIN PROTEIN LC.  
 FT CONFLICT 99 99 H -> R (IN AA SEQUENCE).  
 SQ SEQUENCE 365 AA; 40290 MW; 0FBC0531FB9C0205 CRC64;

Query Match 59.9%; Score 1169; DB 1; Length 365;  
 Best Local Similarity 61.8%; Pred. No. 3.1e-74;  
 Matches 233; Conservative 41; Mismatches 81; Indels 22; Gaps 6;

QY 1 MRSKVLAL--LIPALLAAGAAHAEEYNNKDKNLDLYGKVDGLHYFSNDKNDVGDQTYMR 58  
 DB 1 MKKLITVAISVAASVLAAMSAQAALYNNKDSNKLIDLKGNNAHFFSSNDADDDGDTTYAR 60  
 QY 59 LGFKGETOYTDLTGFGQWEYIOGNSAENENNS--WTRVAFAGLKFQDYGSPDYGRNNG 116  
 DB 61 LGFKGETOINDLTGFGQWEYEFKGNRAESQSSKDKTRLAFAGLKEGDSIDYGRNG 120  
 QY 117 VYVDVTSMTDVLPEFGGDY--GSDNFMQORGNFGATYRTNDFGLVDGLNFAVOYGRKNG 175  
 DB 121 VAYDIGAMTDVLPDEFQDWTQTQDVMTQRTTGFATYRNNDPFGLDGLNFAAOYGRKND 180  
 QY 176 NPSGEGFTSGVTNNGDALRONGDVGSGSTTYDEGFGIGALSSSKRRDAONTAAYT-- 233



RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE OF 1-22 FROM N.A.  
 RX MEDLINE=84297232; PubMed=608911;  
 RA Deutch A.H., Rushlow K.E., Smith C.J.;  
 RT "Analysis of the Escherichia coli PROA locus by DNA and protein  
 sequencing.";  
 RL Nucleic Acids Res. 12:6337-6355(1984).  
 RN [6]  
 RP MUTAGENESIS OF PHE-351.  
 RX MEDLINE=91162638; PubMed=1848301;  
 RA Struyve M., Moons M., Tommassen J.;  
 RT "Carboxy-terminal phenylalanine is essential for the correct assembly  
 of a bacterial outer membrane protein.";  
 RL J. Mol. Biol. 218:141-148(1991).  
 RN [7]  
 RP X-RAY CRYSTALLOGRAPHY (6.0 ANGSTROMS).  
 RX MEDLINE=91172301; PubMed=1848682;  
 RA Jap B.K., Walian P.J., Gehring K.;  
 RT "Structural architecture of an outer membrane channel as determined  
 by electron crystallography.";  
 RL Nature 350:167-170(1991).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).  
 RX MEDLINE=92375189; PubMed=1380671;  
 RA Cowan S.W., Schirmer T., Rummel G., Steiert M., Ghosh R.,  
 Paupilt R.A., Jansonsius J.N., Rosenbusch J.P.;  
 RT "Crystal structures explain functional properties of two E. coli  
 porins.";  
 RL Nature 358:727-733(1992).  
 RN [9]  
 RP TOPOLOGY.  
 RX MEDLINE=93172954; PubMed=7679770;  
 RA Struyve M., Visser J., Adriaanse H., Benz R., Tommassen J.;  
 RT "Topology of Phob porin: the 'eyelet' region.";  
 RL Mol. Microbiol. 7:131-140(1993).  
 CC -1- FUNCTION: THIS IS ONE OF THE PROTEINS INDUCED WHEN E. COLI CELLS  
 ARE GROWN UNDER PHOSPHATE LIMITATION. ITS PROTEIN PORE IS  
 PARTICULARLY EFFICIENT IN THE UPTAKE OF INORGANIC PHOSPHATE,  
 PHOSPHORYLATED COMPOUNDS, AND SOME OTHER NEGATIVELY CHARGED  
 SOLUTES.  
 CC -1- SUBUNIT: HOMOTRIMER.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.  
 CC -1- SIMILARITY: BELONGS TO THE OMP/C/POE FAMILY OF PORINS.  
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 CC -----  
 DR EMBL: V00316; CAA23605.1; -;  
 DR EMBL: D83536; BAA77910.1; -;  
 DR EMBL: AE000132; AAC73345.1; -;  
 DR EMBL: U70214; AAB08661.1; -;  
 DR EMBL: X00786; CAA25362.1; -;  
 DR PIR: A03432; MMECEP.  
 DR PDB: 1PHO; 31-OCT-93.  
 DR SWISS-2DPAGE: P02932; COLI.  
 DR ECO2DBASE: B037.0; 6TH EDITION.  
 DR EcGene: EG10729; POE.  
 DR InterPro: IPR001702; -;  
 DR InterPro: IPR001897; -;  
 DR Pfam: Pf00267; Gram-ve\_porins; 1.  
 DR PRINTS: PR00182; ECOLIPORIN.  
 DR PRINTS: PR00183; ECOLIPORIN.  
 DR PROSITE: PS00576; GRAM\_NEG\_PORIN; 1.  
 KW Outer membrane; Transmembrane; Porin; Signal; 3D-structure.  
 FT SIGNAL 1 21  
 FT CHAIN 22 351  
 FT MUTAGEN 351 351  
 FT OUTER MEMBRANE PORE PROTEIN E.  
 FT F->Y,N,S,V: LESS RESISTANT TO TRYPSIN.

FT STRAND 25 26  
 FT STRAND 30 35  
 FT STRAND 37 45  
 FT STRAND 52 53  
 FT STRAND 56 63  
 FT STRAND 71 82  
 FT STRAND 87 88  
 FT STRAND 93 104  
 FT STRAND 105 107  
 FT STRAND 108 116  
 FT STRAND 119 119  
 FT HELIX 120 123  
 FT TURN 124 126  
 FT TURN 140 141  
 FT TURN 143 145  
 FT STRAND 147 157  
 FT TURN 159 162  
 FT TURN 164 165  
 FT STRAND 166 173  
 FT STRAND 176 176  
 FT TURN 182 183  
 FT STRAND 185 185  
 FT STRAND 188 197  
 FT TURN 198 201  
 FT STRAND 202 212  
 FT HELIX 215 217  
 FT TURN 218 219  
 FT STRAND 227 239  
 FT TURN 240 241  
 FT STRAND 242 252  
 FT STRAND 264 274  
 FT STRAND 280 292  
 FT STRAND 294 294  
 FT TURN 295 297  
 FT STRAND 298 298  
 FT STRAND 301 313  
 FT STRAND 318 327  
 FT TURN 334 335  
 FT STRAND 342 350  
 SQ SEQUENCE 351 AA; 38922 MM; 249E2E362C030C9A CRC64;  
  
 Query Match 56.8%; Score 1109; DB 1; Length 351;  
 Best Local Similarity 58.3%; Pred. No. 4.3e-70;  
 Matches 217; Conservative 53; Mismatches 76; Indels 26; Gaps 9;  
  
 QY 1 MKSVYLLALLPALLAAGAAHAAYVYKNDGKLDLYGKVDGLHYSDNKNVDGDOITYRLG 60  
 DB 1 MKKSTLALVVGIVASASVQAELIYKNDGKLDVYGVKKAHMYSDNASKDGDSYIRFG 60  
 QY 61 FKGETOYTDOLTYGOMPEYTOGNSAENEN-NSWTRVAFAGLKRQDYPFGYGRNYGVY 119  
 DB 61 FKGETQINDOLTYGKRWAEFAGKKAESDTRAQKTRFLAFGLKTRKDGSPFYGRNLGLY 120  
 QY 120 DVTSMYTLVLPFEGSDTYG-SDNFMQORGNFGATYRNTDFGLVLDGLNFAYOGRNGNPS 178  
 DB 121 DVEAMTDMFPEFGSDSSAQTDNFMFKRASGLATYRNTDFGLVLDGLNLTQYQKNE-- 178  
 QY 179 GEGFTSGVTNNGRDALRONGDVGGSITYDEG--FGIGCAISSSKRTDAQNTAAYIGNG 236  
 DB 179 -----RDVKKONGDGFSTSLYDFGGSDFAIISGAYVTRSDRTEQNLOS-GTG 225  
 QY 237 DRAETTYGGLKYDANNNTYLAQYQTYNATRVVSLGMANKRQNEAVAYOQDFGLRPSL 296  
 DB 226 KRAEAMATGLKYDANNNTYLAFTFSETRKMPITG-GRANKQNEAVAYOQDFGLRPSL 284  
 QY 297 AYLOSCKNLGRGYDDILKYVDVGVATYYFNKMSYVDYKILLD-DNQFTRDAGINT 355  
 DB 285 GYVLSKSKDI-EGIGDDELVNYIDVGATYYFNKMSAFVYDKINQSDSKL-----NINN 339  
 QY 356 DNIVALGLVYQF 367  
 DB 340 DDIVAVGMFYQF 351

Tue Aug 21 21:40:18 2001

us-09-575-061-1.rsp

Page 12

Search completed: August 21, 2001, 20:59:41  
Job time: 116 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 21, 2001, 20:57:45 ; Search time 15.97 Seconds  
(Without alignments)  
1750.536 Million cell updates/sec

Title: US-09-575-061-1  
Perfect score: 1953  
Sequence: 1 MRSKVLALLIPALLAGAAH.....TRDAGINTDNIVALGLVYQF 367

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1914	98.0	367	1 MMECP	outer membrane por
2	1804	92.4	367	2 B85861	outer membrane por
3	1539.5	78.8	378	1 MMEBPC	outer membrane por
4	1537	78.7	363	2 S51104	outer membrane por
5	1512.5	77.4	378	1 A59139	outer membrane por
6	1295	66.3	377	2 D64888	outer membrane por
7	1213.5	62.1	394	2 S34263	outer membrane por
8	1177	60.3	365	1 MMECNC	outer membrane por
9	1174	60.1	365	1 MMEBPC	outer membrane por
10	1142.5	58.5	366	2 E85729	probable outer mem
11	1109	56.8	351	1 MMECPC	outer membrane por
12	1109	56.8	351	2 B85113	outer membrane por
13	1104	56.5	362	1 MMECF	outer membrane por
14	1104	56.5	362	2 B85619	outer membrane por
15	1086	55.6	351	2 S25520	outer membrane por
16	1065.5	54.6	350	2 S23525	outer membrane por
17	1055.5	54.0	350	2 S36606	outer membrane por
18	1027.5	52.6	363	2 S43159	outer membrane por
19	1002	51.3	369	2 S70847	outer membrane por
20	733.5	37.6	255	2 D85740	partial probable o
21	732	37.5	315	2 T46933	hypothetical prote
22	692	35.4	224	2 F85814	probable outer mem
23	600	30.7	171	2 H64960	outer membrane por
24	592	30.3	382	2 G84971	ompF-like porin (l
25	522.5	26.8	123	2 C85740	partial probable o
26	478	24.5	191	2 G85814	probable outer mem
27	388.5	19.9	134	2 B64961	outer membrane por
28	310	15.9	96	2 C64900	outer membrane pro
29	279	14.3	350	2 A82299	outer membrane pro

30	254	13.0	331	2 E82389	probable outer mem
31	215.5	11.0	97	2 A57983	outer membrane por
32	194.5	10.0	371	2 S68072	major outer membra
33	194.5	10.0	371	2 S68069	major outer membra
34	176	9.0	386	2 S68062	major outer membra
35	174.5	8.9	326	2 JN0792	major outer membra
36	173.5	8.9	385	2 S68066	major outer membra
37	172.5	8.8	385	2 S68067	major outer membra
38	169.5	8.7	385	2 S68070	major outer membra
39	169	8.7	50	2 T46990	hypothetical prote
40	168.5	8.6	361	2 JC6314	major porin protei
41	165	8.4	330	2 PC4425	lectin-like adhesi
42	164.5	8.4	361	2 A30542	major outer membra
43	163.5	8.4	359	2 D64050	major outer membra
44	156.5	8.0	368	2 A82148	probable porin VC1
45	155	7.9	360	2 S17456	outer membrane pro

## ALIGNMENTS

RESULT 1

MMECP

C:Species: Escherichia coli

C>Date: 31-Dec-1990 #sequence-revision 31-Dec-1990 #extl-change 16-Jul-1999

C:Accession: A20867; A18885; B25029; E64991

R:Mizuno, T.; Chou, M.Y.; Inouye, M.

J. Biol. Chem. 258, 6932-6940, 1983

A>Title: A comparative study on the genes for three porins of the Escherichia coli ou

A:Reference number: A20867; MUID:83213433

A:Accession: A20867

A:Molecule type: DNA

A:Residues: 1-367 <MIZ>

A:Cross-references: GB:K00541; GB:M10314; GB:M14188; NID:g147007; PIDN:AAA24243.1; PI

R:Mizuno, T.; Chou, M.Y.; Inouye, M.

FEBS Lett. 151, 159-164, 1983

A>Title: DNA sequence of the promoter region of the ompC gene and the amino acid sequ

A:Reference number: A18885; MUID:83132326

A:Accession: A18885

A:Molecule type: DNA

A:Residues: 1-40 <MIZ>

R:Nogami, T.; Mizuno, T.; Mizushima, S.

J. Bacteriol. 164, 797-801, 1985

A>Title: Construction of a series of ompE-ompC chimeric genes by in vivo homologous r

A:Reference number: A91809; MUID:86033642

A:Accession: B25029

A:Molecule type: DNA

A:Residues: 32-57 <NOG>

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;

A:Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A>Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617

A:Accession: E64991

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-367 <BLAT>

A:Cross-references: GB:AE000310; GB:U00096; NID:g2367131; PIDN:AACT5275.1; PID:g17885

A:Experimental source: strain K-12, substrain MG1655

A:Gene: ompC

A:Map position: 47 min

C:Function:

A:Description: one of the E. coli major outer membrane proteins that form passive dif

C:Superfamily: outer membrane protein por

C:Keywords: membrane protein; porin; trimer

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-367/Product: outer membrane porin ompC #status predicted <MAT>

Query Match 98.0%; Score 1914; DB 1; Length 367;

Best Local Similarity 98.1%; Pred. No. 5,6e-127;

	Matches	360;	Conservative	3;	Mismatches	4;	Indels	0;	Gaps	0;
QY	1	MKSKYVLLALLPALLAAGAAHAAEYVNNKDGCKIDLTKYVDGLHYESDNKDFVDGDTYMRIG	60							
	1									
	1	MKVYVLSLIVPALPVLVAGANAAEYVNNKDGCKIDLTKYVDGLHYESDNKDFVDGDTYMRIG	60							
QY	61	FKGEQVYVDLDTLGVGOWEIOIGNSAENENNSWTFVAFAGLKFOVVGSPDGRNRYGYVD	120							
	61									
Dp	61	FKGEQVYVDLDTLGVGOWEIOIGNSAENENNSWTFVAFAGLKFOVVGSPDGRNRYGYVD	120							
QY	121	VTSWTDVLPFEFGDITGYGSDNFMQORGNFGATYRNTDFGLVDGLNFAYOYOGKGNPSSGE	180							
	121									
Dp	121	VTSWTDVLPFEFGDITGYGSDNFMQORGNFGATYRNTDFGLVDGLNFAYOYOGKGNPSSGE	180							
QY	181	GFTSCVTVNNGRDALRQNDGVGSGITTYDEEGFGIGGALISSKRTDAQNTAAITNGDRAE	240							
	181									
Dp	181	GFTSCVTVNNGRDALRQNDGVGSGITTYDEEGFGIGGALISSKRTDAQNTAAITNGDRAE	240							
QY	241	TYTGLGLKTDANNITVLAAYOTQTYNATRVGSLGWMAKKAONFEVVAOYQDFGIRPSLATIQQ	300							
	241									
Dp	241	TYTGLGLKTDANNITVLAAYOTQTYNATRVGSLGWMAKKAONFEVVAOYQDFGIRPSLATIQQ	300							
QY	301	SKGKNLGRGYDEDEILKYVDVGATYFNKNMSTYVDYKINLDDNQFTPDAGINTDNITVA	360							
	301									
Dp	301	SKGKNLGRGYDEDEILKYVDVGATYFNKNMSTYVDYKINLDDNQFTPDAGINTDNITVA	360							
QY	361	LGIVYQF	367							
	361									
Dp	361	LGIVYQF	367							

```

RESULT      2
8B5861
outer membrane protein 1b (lbc) [imported] - Escherichia coli (strain O157:H7)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C:Accession: B85861
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D. J.; Mayhew  

Miller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Diallantha, E.; Potamoustis, K.; Apodaca  

Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7 .
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: B85861
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-367 <SMD>
A:Cross-references: GB:AA005174; NID:g12516550; PIDN:ANG57350.1; GSPDB:GN00145; UWGP:Z33  

A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: ompC
;Superfamily: outer membrane protein phoc

```

Query Match	92.4%	Score 1804	DB 2	Length 367	
Best Local Similarity	92.5%	Pred. No. 2.9e+119			
Matches 343	Conservative	9	Mismatches 11	Indels 8	Gaps 2
QY	1	MKSKVALLIIPALLAAGAAHAAEYVNNKDKNKLDTLGKVDGLHTEFSDNKDQVDDQTYMRLG	60		
		1	MKVKVLSTLVPALVAAGANAAYNNKDKNKLDTLGKVDGLHTEFSDDKSYDDQTYMRLG	60	
Db					
QY	1	FKGEQVYDQDLTGYGQWMEYQIQGNSAENENNSWPTVAAGLKFQVQGSFDYGRNTGVYVD	120		
		61	FKGEQVYDQDLTGYGQWMEYQIQGNSAENENNSWPTVAAGLKFQVQGSFDYGRNTGVYVD	120	
Db					
		61	FKGEQVYDQDLTGYGQWMEYQIQGNSAENENNSWPTVAAGLKFQVQGSFDYGRNTGVYVD	120	
QY	121	VTSMYDVLPEFGGDPYGSDFNFMQGRNGATYRNTDFEGLVDGLNFAVQYQGGKNGNPSGE	180		
		121	VTSMYDVLPEFGGDPYGSDFNFMQGRNGATYRNTDFEGLVDGLNFAVQYQGGKNGNPSGE	180	
Db					
QY	181	GFTSGVTNNKGDALRQNDQYGGSGITTYDEGFGICGALISSKRTDQNTAAATIGGDAE	240		
		181	---GMTNNGEALRQNDQYGGSGITTYDEGFGICAAAYSSKRTDDQNSPLYTIGGDAE	236	

Oy	241	TYTGGLKTDANNITLLAAYOTQTYNATRVGSLGAMNKAKQNEPAVAQYQFPDGLSPSLAYIQ	3000
Db	237	TYTGGLKTDANNITLLAAYOTQTYNATRVGSLGAMNKAKQNEPAVAQYQFPDGLRSLAYIQ	2966
Oy	301	SKGKRL----GRGVDDDEDILKYVDVGATPYENKMKSTYVDYKINLLDDNQFTRDAGINTD	3566
Db	297	SKGKRLGVINIRNRYDDDEDILKYVDVGATPYENKMKSTYVDYKINLLDDNQFTRDAGINTD	3566
Oy	357	NIVALGLVYQF 367	
Db	357	NIVALGLVYQF 367	

outer membrane porin ompC precursor - Salmonella typhi  
 C:Species: Salmonella typhi  
 C:Date: 31-Dec-1990 #sequence-revision 31-Dec-1990 #text-change 16-Jul-1999  
 C:Accession: J00119; S01248; S10122  
 R:Puentes, J.L.; Alvarez-Scherer, V.; Gosset, G.; Calva, E.  
 Gene 83, 197-206, 1989  
 A:Title: Comparative analysis of the Salmonella typhi and Escherichia coli ompC genes  
 A:Reference number: J00119; M0UD:90060831

A:Cross-references: GB:M31424; NID:g154207; PIDN:AAA27169.1; PID:g154208  
R:Venegas, A.; Gomez, I.; Zorov, I.; Yudelevich, A.  
Nucleic Acids Res. 16, 7721, 1988  
A:Title: The nucleotide sequence of the *Salmonella typhi* ompC porin gene  
A:Reference number: S01248; MUID:88319959  
A:Accession: S01248  
A:Molecule type: DNA  
A:Residues: 1-5,'G','7-361,363-378 <VEN2>  
A:Cross-references: EMBL:X07835; NID:g47796; PIDN:CAA30688.1; PID:g47797  
A:Experimental source: strain Ty2  
R:Venegas, A.  
Submitted to the EMBL Data Library, May 1988  
A:Reference number: S10122  
A:Accession: S10122  
A:Molecule type: DNA  
A:Residues: 1-361,363-378 <VEN2>  
A:Cross-references: EMBL:X07835; NID:g47796; PIDN:CAA30688.1; PID:g47797  
A:Genetics:  
A:Gene: ompC  
A:Map position: 45 min  
C:Superfamily: outer membrane protein phos  
C:Keywords: membrane protein; porin; trimmer  
E:1-21/Domain: signal sequence #status predicted <SIG>  
E:22-378/Product: outer membrane porin ompC #status predicted <MAT>

	Query Match	78.8%	Score 1539.5:	DB 1;	Length 378;	
	Best Local Similarity	77.3%:	Pred No.1e-100;			
	Matches 297;	Conservative 24;	Mismatches 40;	Indels 23;	Gaps 5;	
Qy	1 M K S K V L A L L I P A L L A G A H A E V Y N K D G N K L D L G K V D G L H F S D N K D V D G D Q Y T M R L G	60				
Db	1 M K V K L S I L P A L L A V A G A N A E I Y N K G D N K L D L G K V G L H F S D D K S P D Q Y T M R I G	60				
Qy	61 F K G E Q V A N D L O L T G C W E M E Y O I O G N S A E N N E N S W T F A P F L G F E O V G S P D Y R N T G V V D	120				
Db	61 F K G E T V A N D Q L G T G W E M E Y O I O G N T E G S N D S W T R F A F L G F A D A G S T D Y G R N T G V T D	120				
Qy	121 V T S W T D L P L E F E G D Y T G S D N F M Q O R G N F G A Y R N T D F E G L V D G L N F A V O Y G K N G N P S G E	180				
Db	121 V T S W T D L P L E F E G G D Y T G A D N F M Q O G R G N G A Y A T R N T D F E G L V D G L D F A L O Y O Q R K N G S V S G E	180				
Qy	181 G F T S V T N N G R A L N O N D D Y G G S I T T Y D - E E F G I G A L I S S K K R P D A O N T A --- Y I N G	236				
Db	181 ----- N T N G R S L N O N D D Y G G S I T T A I G E F S V G A L T T S K R P A D O N N T A N A R L Y G N G	234				
Qy	237 D R A E Y T T G L K D A N N I Y L A O Y T O T Y A N T R G ----- S L G W A N K A Q N F E A V A O Y O	287				

```

Db 235 DRAVYVYTGGLYDANNIYLAQYQSYQATNATRFGTSGNSNPSTSGFANKQNFVVAQYQ 294
OY 288 FDFGLRPSLAYLQSKGNLGRG----YDDEDILKYVDVGATYYFNKMNSTYVDKINLDD 343
Db 295 FDFGLRPSVAYLQSKGDIISNGYASGYDODIVKYVDGATYYFNKMNSTYVDKINLDD 354
OY 344 DNOFTRDAGINTDNIVALGLVYQF 367
Db 355 KNDFTRDAGINTDIDIVALGLVYQF 378

```

## RESULT 4

outer membrane porin ompK36 precursor - Klebsiella pneumoniae

C:Species: Klebsiella pneumoniae  
C:Date: 07-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 20-Aug-1999  
C:Accession: S51104  
R:Alberti, S.  
Submitted to the EMBL Data Library, May 1994  
A:Description: A porin from Klebsiella pneumoniae: sequence homology, three-dimensional  
A:Reference number: S51104  
A:Accession: S51104  
A:Molecule type: DNA  
A:Residues: 1-363 <ALB>  
A:Cross-references: EMBL:233506; NID:g2104843; PIDN:CAA83913.1; PID:g619891  
C:Genetics:  
A:Gene: ompK36  
A:Superfamily: outer membrane protein phoE  
C:Keywords: membrane protein; porin; trimer  
F:1-21/Domain: signal sequence #status predicted <Sig>  
F:22-363/Product: outer membrane porin ompK36 #status predicted <Mat>

Query Match 78.7%; Score 1537; DB 2; Length 363;

Best Local Similarity 78.9%; Pred. No. 1.5e-100;  
Matches 291; Conservative 32; Mismatches 38; Indels 8; Gaps 5;

```

OY 1 MRSKVALLIPALLAAGAAHAAYEYNNKDKNKLDELGYKVDGLHPSDNKDDVDGDOTYKRLG 60
Db 1 MKYVLSLVPALLVAGANAAAEIYNNKDKNKLDELGYKVDGLHPSDNKDDVDGDOTYKRLG 60
OY 61 FKGETQVTDLTGYGQWEYQIOGNSAENENN-SWTRVAFAGLKFQDVSGFDYGRNYGVY 119
Db 61 VKGETQINDLTGYGQWEYNNQANTSESSDQAWTRLAFAGLKFQDVSGFDYGRNYGVY 120
OY 120 DVTSMVTDLPEFGDGTYSNDFNQKRGNFAGATYRNTDFEGLVDGLNFAVQYQKNGNPSG 179
Db 121 DVTSMVTDLPEFGDGTYSNDFNQKRGNFAGATYRNTDFEGLVDGLNFAVQYQKNGSVSG 180
OY 180 EGFSGVTNNGRDALRONGDVGSGITYD-YEGFGIGAISSSKRTDAONTAAIYINGDR 238
Db 181 E----GATNNGRGALKNKGSGFGTSYTDIEDGISAGFAVANSKRTDQDQ--QLLLGSDH 235
OY 239 AEITYTGLKTDANNIYLAQYQSYQATNATRVGSLGMANKAONEVAAYQFDFGLRPSLAY 298
Db 236 AEITYTGLKTDANNIYLAQYQSYQATNATRVGSLGMANKAONEVAAYQFDFGLRPSLAY 295
OY 299 LOSGKMLGSGYDDEDILKYVDVGATYYFNKMNSTYVDYKINLDDNQFPRDGINNDI 358
Db 296 LOSGKMLGSGYDDEDILKYVDVGATYYFNKMNSTYVDYKINLDDNQFPRDGINNDI 354
OY 359 VALGLVYQF 367
Db 355 VALGLVYQF 363

```

## RESULT 5

outer membrane porin C precursor - Salmonella typhimurium

N:Alternate names: ompC protein  
C:Species: Salmonella typhimurium  
C:Date: 12-Nov-1999 #sequence\_revision 12-Nov-1999 #text\_change 12-Nov-1999

C:Accession: A59139  
R:Negm, R.S.; Pistole, T.G.  
Can. J. Microbiol. 45, 658-669, 1999  
A:Title: The porin OmpC of Salmonella typhimurium mediates adherence to macrophages.  
A:Reference number: A59139; MUID:99457705  
A:Accession: A59139  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-378 <NEG>  
A:Cross-references: GB:AF039309; NID:g2773086; PIDN:AB96675.1; PID:g2773087  
A:Experimental source: strain 14028  
A:Note: submitted to GenBank, December 1997  
C:Genetics:  
A:Gene: ompC  
A:Map position: 49.3 minutes  
C:Complex: homotrimer  
C:Superfamily: outer membrane protein phoE  
C:Keywords: homotrimer; membrane protein; porin  
F:1-21/Domain: signal sequence #status predicted <Sig>  
F:22-378/Product: outer membrane porin ompC #status predicted <Mat>

Query Match 77.4%; Score 1512.5; DB 1; Length 378;  
Best Local Similarity 76.6%; Pred. No. 8e-99;  
Matches 294; Conservative 26; Mismatches 41; Indels 23; Gaps 6;

```

OY 1 MRSKVALLIPALLAAGAAHAAYEYNNKDKNKLDELGYKVDGLHPSDNKDDVDGDOTYKRLG 60
Db 1 MKYVLSLVPALLVAGANAAAEIYNNKDKNKLDELGYKVDGLHPSDNKDDVDGDOTYKRLG 60
OY 61 FKGETQVTDLTGYGQWEYQIOGNSAENENN-SWTRVAFAGLKFQDVSGFDYGRNYGVYD 120
Db 61 FKGETQVNDLTGYGQWEYQIOGNOTEGSNDSTWTRVAFAGLKFADAGSPDYGRNYGVYD 120
OY 121 VTSMTDVLPEFGDGTYSNDFNQKRGNFAGATYRNTDFEGLVDGLNFAVQYQKNGNPSGE 180
Db 121 VTSMTDVLPEFGDGTYSNDFNQKRGNFAGATYRNTDFEGLVDGLNFAVQYQKNGSVSGE 180
OY 181 GFPSGVTNNGRDALRONGDVGSGITYD-YEGFGIGAISSSKRT-DAONT--AAIYING 236
Db 181 -----NTNGRSLNNGDGGYSLIYAIIEGFSVGAITTSKRTADQDNTANRLYNG 234
OY 237 DRAETTYGLKTYDANNIYLAQYQSYQATNATRVG-----SLGMANKAONEVAAYQY 287
Db 235 DRAVYVYTGGLYDANNIYLAQYQSYQATNATRVGSGNSNPSTSGFANKQNFVVAQYQ 294
OY 288 FDFGLRPSLAYLQSKGNLGRG----YDDEDILKYVDVGATYYFNKMNSTYVDKINLDD 343
Db 295 FDFGLRPSVAYLQSKGDIISNGYASGYDODIVKYVDGATYYFNKMNSTYVDKINLDD 354
OY 344 DNOFTRDAGINTDNIVALGLVYQF 367
Db 355 KYEFTRDAGINTDIDIVALGLVYQF 378

```

## RESULT 6

outer membrane porin b1377 precursor - Escherichia coli

C:Species: Escherichia coli  
C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 20-Aug-1999  
C:Accession: D64888  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;  
A.: Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; MUID:97426617  
A:Accession: D64888  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-377 <BLAT>

A:Cross-references: GB:AE000234; GB:U00096; NID:g1787633; PIDN:AACT4459.1; PID:g17876  
A:Experimental source: strain K-12, substrain MG1655  
C:Superfamily: outer membrane protein phoE

C:Keywords: membrane protein; porin; trimer  
F:1-21/Domain: signal sequence #status predicted <Sig>  
F:22-377/Product: probable outer membrane porin b1377 #status predicted <Opp>

Query Match 66.3%; Score 1295; DB 2; Length 377;

Best Local Similarity 67.8%; Pred. No. 1.4e-83;

Matches 261; Conservative 37; Mismatches 61; Indels 26; Gaps 10;

```

QY 1 MKRKVALLLIPALLAAGAAHAAYNNKDGKLLDYGKVDLHFSDNKKVDGQDTYKRLG 60
    |||||
DB 1 MKRKVALLLIPALLAAGAAHAAYNNKDGKLLDYGKVDLHFSDNKADGQDSYARLG 60
    |||||

QY 61 FKGETVDTDLTGCGMEYOIQGNSAE-NEENNSMTRYAFGLKFDQDGFYRNGVY 119
    |||||
DB 61 FKGETQINDLTGCGMEYIQGNNTESSKQNSMTSLAFGLKFDYGSIDYRNGVY 120
    |||||

QY 120 DVTSMVDLPEFGDITY-GSDNFMQGRNGFATYRMTDFGLVDGLFAVOYQGNKNS 178
    |||||
DB 121 DIGMTDMLPEFGDSTYNADNEMTGANGVATYRMTDFGLVNGLFAVOYQGN- 176
    |||||

QY 179 GEGFTGSV--TNNGRDLRNGDGVGSITYDY-EGTGIGALISSKRTDAQ--NTRAYI 233
    |||||
DB 177 -EGASNGQEGTNGRDVNRHENGSGWGLSTYDGLGMGFSAGAAATSSDRTDQVNHTRAA- 233
    |||||

QY 234 GNGDRATETTYGGLKYDANNITYLAQYTOTYNTATRVGSLGW--ANKAQNFPAVAOYQDFG 291
    |||||
DB 234 -GGDKKADMTAGLKYDANNITYLATMYSETRNMTPEFGSDSYAVANKTONFEVTAQYQDFG 292
    |||||

QY 292 LRPSLAYLQSKGNL-----GREYDEDLIKYVDGATYFFNKNMSTYVDYKINLMD 343
    |||||
DB 293 LRPAVSFLMSKGRDLHAAGADNPAGVDKDLVKADIGATYFFNKNMSTYVDYKINLMD 352
    |||||

QY 344 -DNOGTRDAGINTDNTVALGLVYQF 367
    |||||
DB 353 EDDSFYAANGISTYDVALGLVYQF 377
    |||||

```

# RESULT 7

S34263

outer membrane porin ompF precursor - Salmonella typhi

C:Species: Salmonella typhi

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 20-Aug-1999

C:Accession: S34263

R:fernandez-Mora, M.; Calva, E.

Submitted to the EMBL Data Library, June 1993

A:Reference number: S34263

A:Accession: S34263

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-394 <FER>

A:Cross-references: EMBL:X7327; NID:g602362; PIDN:CAA51710.1; PID:g311957

C:Genetics:

A:Gene: ompF

C:Superfamily: outer membrane protein phoe

C:Keywords: membrane protein; porin; trimer

F:1-21/Domain: signal sequence #status predicted <Sig>

F:22-394/Product: outer membrane porin ompF #status predicted <Mat>

Query Match 62.1%; Score 1213.5; DB 2; Length 394;

Best Local Similarity 62.8%; Pred. No. 7.5e-78;

Matches 248; Conservative 38; Mismatches 80; Indels 29; Gaps 10;

```

QY 1 MKRKVALLLIPALLAAGAAHAAYNNKDGKLLDYGKVDGLHFSDNKKVDGQDTYKRLG 60
    |||||
DB 1 MKRKVALLLIPALLAAGAAHAAYNNKDGKLLDYGKVDGLHFSDNKADGQDSYARLG 60
    |||||

QY 61 FKGETVDTDLTGCGMEYOIQGNSAENEN-NSMTRYAFVAGLGFQDQGFYRNGVY 119
    |||||
DB 61 FKGETQINDLTGCGMEYIKYNTTEGEGANSMTSLAFGLKFDYGSIDYRNGVY 120
    |||||

QY 120 DVTSMVDLPEFGDITY-GSDNFMQGRNGFATYRMTDFGLVDGLFAVOYQGNKNS 178
    |||||

```

```

DB 121 DIRMATDMLPEFGDITYQTDVYMLGRNCGVATYRMTDFGLVGLNFAVOYQGNEN-G 179
    |||||
QY 179 GEGFTGSVTNNG-RDLRONGDVGGSITYDYE-GGIGALISSKRTDAQNAT- 232
    |||||
DB 180 GAGAGDGTGNGKRLARENGDGFSGMSTSYDFGLGSLGAAYSSDSRSDNQVARGDGM 239
    |||||
QY 233 -----TGNCRATETTYGGLKYDANNITYLAQYTOTYNTATRV-----GSLGMANKQNF 281
    |||||
DB 240 NEENNSMTRYAFGLKFDQDGFYRNGVY-ETRNMTYGGGNGEGNSINKTQNE 299
    |||||

QY 282 AVAQYQDFGLRPSLAYLQSKGNLQ-----RG---YDEDLIKYVDGATYFFNKNMST 333
    |||||
DB 300 VVAQYQDFGLRPSLAYLQSKGKDLGQEVHRGNMERTDKDLVKYVDGATYFFNKNMST 359
    |||||

QY 334 YVDYKINLMD-DNOGTRDAGINTDNTVALGLVYQF 367
    |||||
DB 360 YVDYKINLMDDEDDFYANNIGATDIDVGLVYQF 394
    |||||

```

# RESULT 8

M5CNC

outer membrane porin mmpC precursor - Escherichia coli cryptic lambdoid prophage DLP1

C:Species: Escherichia coli

C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Jul-1999

C:Accession: A25647; S66594; G64787

R:Blasband, A.J.; Marcotte Jr., W.R.; Schnaitman, C.A.

J. Biol. Chem. 261, 12723-12732, 1986

A:Title: Structure of the Ic and mmpC outer membrane porin protein genes of lambdoid

A:Reference number: A25647; MUID:86304457

A:Contents: mutant strain CS384

A:Accession: A25647

A:Molecule type: DNA

A:Residues: 1-365 <BLA>

R:Mandl, A.A.; Sharples, G.J.; Mandel, T.N.; Lloyd, R.G.

J. Mol. Biol. 257, 561-573, 1996

A:Title: Holliday junction resolvases encoded by homologous rusa genes in Escherichia

A:Reference number: S66579; MUID:96196428

A:Accession: S66594

A:Molecule type: DNA

A:Residues: 347-365 <MAN>

A:Cross-references: EMBL:X92587; NID:g1051136; PIDN:CAA63325.1; PID:g1051145

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.

A.; Rose, D.J.; Mau, B.; Sho, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617

A:Accession: G64787

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 'MNTYRAVTSFNNSSKGLT', 1-325, 'N', 327-347, 'EGANKSLI' <BLAT>

A:Cross-references: GB:AE000160; GB:U00096; NID:g1786751; PIDN:AAC73654.1; PID:g17867

A:Experimental source: strain K-12, substrain MG1655

C:Comment: in wild-type strains of E. coli K-12, the mmpC open reading frame is inter

ain CS348, the IS5 element has been deleted and mmpC is expressed.

C:Genetics:

A:Gene: mmpC

A:Map position: 12 min

A:Genome: cryptic lambdoid prophage DLP12

C:Superfamily: outer membrane protein phoe

C:Keywords: membrane protein; porin; trimer

F:1-23/Domain: signal sequence #status predicted <Sig>

F:24-365/Product: outer membrane porin mmpC #status predicted <Mat>

Query Match 60.3%; Score 1177; DB 1; Length 365;

Best Local Similarity 62.1%; Pred. No. 2.5e-75;

Matches 234; Conservative 41; Mismatches 80; Indels 22; Gaps 6;

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QY 1 MKSKVAL--LIPALLAAGAAHAAYNNKDGKLLDYGKVDGLHFSDNKKVDGQDTYKRLG 58
    |||||
DB 1 MKKLTVAISVAASVLAASQAABEITYKDSNKLDTLGYKVNNAKHFSSNDADDDGDTTAK 60
    |||||

```



[illegible]

```

Query March 58.5%; Score 1142.5; Db 2; Length 366;
Best Local Similarity 59.98; Pred. No. 6,56-73;
Matches 226; Conservative 45; Mismatches 85; Indels 21; Gaps 6;

QY 1 M K S V A L L I P A L L A G A A H A E V Y N K D G N K L D Y G K V D G L H Y F S D N K O V D G D O T Y M R L G 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 M K L I V A V V V V G L L A A N V A H A A E V Y N K D G N K L D Y G K T A L R Y F T D D K R D G D K T Y A R L G 60

QY 61 F K G E V V I D O L T G Y G O M E Y O I G - - N S A E N N S M S T W R A F A G L E F O D G S P D Y G R N Y C V V 118
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 F K G E T O I D D O M I G G H M E Y D R K G Y N D E A N G S R D N K T R I A Y A G L K I S E G S I D Y G R N Y V G 120

QY 119 Y D V T S W T D V L P E F G G D T Y G - S D N F M O O R G N G A Y R N T D F F G L V D G L N F A V O Y O G K N G N P 177
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Db 121 Y D I S W T D M L P E F G G D T Y S O K D V F E M T Y R T T G V A Y R N D F E G L L E G L F A A Y O G K N R - 179

QY 178 S G E F T S G V T N - - - - G R D A L R O N G D G G S I T Y D E S E F G I G A I S S K R F D A O N T A A - - 231
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 180 - - - - - - - - - - I D N S H L Y G A D I T R A N G D G F G I S T Y Y D E F G I G A Y T T S D R I N A O B R A A N 230

QY 232 - Y I G N D R A E T Y T G L K R Y D A N N I T L A A Q Y T O T Y N A T R V G S L G M A N K A O N F E A V A O Y O F D F 290
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 231 P L N S G K N A E L M A G I K R D A N N I Y F A A N Y A E T L N M T Y T G D G Y I S N K A O S F E V A O Y O F D F 290

QY 291 G L R S L A Y I O S K G N L K R G Y D E D I L K R Y D V G A Y Y E F N K N S T V D Y K I N L L D N O F R D 350
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 291 G L R S L A Y L K S K G I D L G R - Y G D O D M I E I D V G A T F F K N N S T Y V D I K I N L I D E S D F T R A 349

QY 351 A G I N T D I V A L G L Y V O F 367
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 350 V D I R T D N I V A T G I T Y O F 366

RESULT 11
MMECPe
outer membrane porin phoE precursor - Escherichia coli
C:Species: Escherichia coli
C:Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C:Accession: A03432; B64749
R:Overbeek, N.; Bergmans, H.; van Mansfeld, F.; Lugtenberg, B.
J. Mol. Biol. 163, 513-532, 1983
A:Title: Complete nucleotide sequence of phoE, the structural gene for the phosphate
A:Reference number: A92893; MUID:83189086
A:Accession: A03432

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 21, 2001, 20:57:45 ; Search time 12.35 Seconds  
(without alignments)  
611.875 Million cell updates/sec

Title: US-09-575-061-1

Perfect score: 1953  
Sequence: 1 MKSKVLALLPALLAGAAH.....TRDAGINTNIVALGLVYQF 367

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PCATUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/Dackfilest1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1914	98.0	367	US-09-041-889-30	Sequence 30, Appl
2	1285	65.8	377	US-09-041-889-29	Sequence 29, Appl
3	1078.5	55.2	323	US-09-041-889-28	Sequence 28, Appl
4	1027	52.6	340	US-08-355-844-1	Sequence 1, Appl
5	1027	52.6	340	PCT-US95-16126-1	Sequence 1, Appl
6	164.5	8.4	361	US-08-096-181A-8	Sequence 8, Appl
7	164.5	8.4	361	PCT-US94-08326-8	Sequence 8, Appl
8	140.5	7.2	342	US-08-096-182A-4	Sequence 4, Appl
9	140.5	7.2	342	US-08-877-109-4	Sequence 4, Appl
10	140.5	7.2	342	US-08-798-760-4	Sequence 4, Appl
11	140.5	7.2	342	PCT-US94-08327-4	Sequence 4, Appl
12	140.5	7.2	363	US-08-096-182A-6	Sequence 6, Appl
13	140.5	7.2	363	US-08-877-109-6	Sequence 6, Appl
14	140.5	7.2	363	US-08-798-760-6	Sequence 6, Appl
15	140.5	7.2	363	PCT-US94-08327-6	Sequence 6, Appl
16	128.5	6.6	589	US-09-377-155-19	Sequence 19, Appl
17	127.5	6.5	363	US-08-096-181A-10	Sequence 10, Appl
18	127.5	6.5	363	PCT-US94-08326-10	Sequence 10, Appl
19	126.5	6.5	342	US-08-096-181A-12	Sequence 12, Appl
20	126.5	6.5	342	US-08-096-181A-14	Sequence 14, Appl
21	126.5	6.5	342	PCT-US94-08326-14	Sequence 14, Appl
22	124.5	6.4	511	US-08-480-604A-20	Sequence 20, Appl
23	124.5	6.4	511	US-08-480-604A-21	Sequence 21, Appl
24	124.5	6.4	608	US-08-405-496A-20	Sequence 20, Appl
25	124.5	6.4	608	US-08-480-604A-21	Sequence 21, Appl
26	124.5	6.4	608	US-08-405-496A-21	Sequence 21, Appl
27	124.5	6.4	609	US-08-480-604A-30	Sequence 30, Appl

28	124.5	6.4	2366	1	US-08-480-604A-10	Sequence 10, Appl
29	124.5	6.4	2366	2	US-08-405-496A-10	Sequence 10, Appl
30	118.5	6.1	309	1	US-08-096-182A-2	Sequence 2, Appl
31	118.5	6.1	309	1	US-08-877-109-2	Sequence 2, Appl
32	118.5	6.1	309	3	US-08-798-760-2	Sequence 2, Appl
33	118.5	6.1	309	5	PCT-US94-08327-2	Sequence 2, Appl
34	116.5	6.0	598	4	US-09-377-155-5	Sequence 5, Appl
35	113.5	5.8	592	4	US-09-377-155-17	Sequence 17, Appl
36	113.5	5.8	594	4	US-09-377-155-15	Sequence 15, Appl
37	112.5	5.8	594	4	US-09-377-155-7	Sequence 7, Appl
38	112.5	5.8	1657	3	US-09-057-570-2	Sequence 2, Appl
39	112.5	5.8	1805	3	US-09-057-570-7	Sequence 7, Appl
40	111.5	5.7	398	4	US-09-377-155-13	Sequence 13, Appl
41	111	5.7	3031	1	US-07-689-008-2	Sequence 2, Appl
42	110.5	5.7	591	4	US-09-377-155-11	Sequence 11, Appl
43	110.5	5.7	591	4	US-09-377-155-21	Sequence 21, Appl
44	110.5	5.7	592	4	US-09-377-155-2	Sequence 2, Appl
45	110	5.6	341	2	US-08-538-711A-8	Sequence 8, Appl

#### ALIGNMENTS

RESULT 1  
US-09-041-889-30  
Sequence 30, Application US/09041889  
Patent No. 6033864  
GENERAL INFORMATION:  
APPLICANT: Braun, Jonathan  
APPLICANT: Conavy, Ofer  
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of  
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using  
TITLE OF INVENTION: Microbial UC PANCA antigens  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/041,889  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/837,058  
FILING DATE: 11-APR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-PW 3006  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9601  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 367 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
US-09-041-889-30

Query Match 98.0% Score 1914; DB 3; Length 367;  
Best Local Similarity 98.1%; Pred. No. 1,4e-157;  
Matches 360; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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QY 1 MRSKVALLIPALLAAGAAHAEVYKDKNKLIDYGVKDLHYFSDNKKVDGQDTYMRIG 60
  1 MKYKVLILVLPALLVAGAAHAEVYKDKNKLIDYGVKDLHYFSDNKKVDGQDTYMRIG 60
Db 1 MKYKVLILVLPALLVAGAAHAEVYKDKNKLIDYGVKDLHYFSDNKKVDGQDTYMRIG 60
QY 61 FKGETVTOQLTGYGQWEOIQGNSAENENSWTRAFALCKQDVGSFPGYGRNYGVYD 120
  61 FKGETVTOQLTGYGQWEOIQGNSAENENSWTRAFALCKQDVGSFPGYGRNYGVYD 120
Db 61 FKGETVTOQLTGYGQWEOIQGNSAENENSWTRAFALCKQDVGSFPGYGRNYGVYD 120
QY 121 VTSMTDVLPEFGGDTYGSDFMOQRNGFATYRNTDFEGLVDGLNFAVOYQGNKNGPSGE 180
  121 VTSMTDVLPEFGGDTYGSDFMOQRNGFATYRNTDFEGLVDGLNFAVOYQGNKNGPSGE 180
Db 121 VTSMTDVLPEFGGDTYGSDFMOQRNGFATYRNTDFEGLVDGLNFAVOYQGNKNGPSGE 180
QY 181 GFISGVTNNRDLRONGDVGGSITYDEFGSIGAIISSSKRTDAONTAAYIGNGDRAE 240
  181 GFISGVTNNRDLRONGDVGGSITYDEFGSIGAIISSSKRTDAONTAAYIGNGDRAE 240
Db 181 GFISGVTNNRDLRONGDVGGSITYDEFGSIGAIISSSKRTDAONTAAYIGNGDRAE 240
QY 241 TYTSGLYKVDANNITYLAOYQOTYNATRVGSLGNANKAONEAVALQOFDEGLRPSLAYIQ 300
  241 TYTSGLYKVDANNITYLAOYQOTYNATRVGSLGNANKAONEAVALQOFDEGLRPSLAYIQ 300
Db 241 TYTSGLYKVDANNITYLAOYQOTYNATRVGSLGNANKAONEAVALQOFDEGLRPSLAYIQ 300
QY 301 SKGKNLGRGYDEDLIKYVDVATYFNKMSYVDYKINLDDNOFTRDAGINTDNIYA 360
  301 SKGKNLGRGYDEDLIKYVDVATYFNKMSYVDYKINLDDNOFTRDAGINTDNIYA 360
Db 301 SKGKNLGRGYDEDLIKYVDVATYFNKMSYVDYKINLDDNOFTRDAGINTDNIYA 360
QY 361 LGLVYQF 367
  361 LGLVYQF 367
Db 361 LGLVYQF 367

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## RESULT 2

US-09-041-889-29

Sequence 29, Application US/09041889

Patent No. 6033864

GENERAL INFORMATION:

APPLICANT: Braum, Jonathan

APPLICANT: Cohay, Offer

TITLE OF INVENTION: Diagnosis, Prevention and Treatment of

TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using

TITLE OF INVENTION: Microbial UC PANCA antigens

NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell &amp; Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/041,889

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/837,058

FILING DATE: 11-APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-PM 3006

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:

LENGTH: 377 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

INFORMATION FOR SEQ ID NO: 28:

US-09-041-889-29

Query Match 65.8%; Score 1285; DB 3; Length 377;  
 Best Local Similarity 67.3%; Pred. No. 2,8e-103;  
 Matches 259; Conservative 38; Mismatches 62; Indels 26; Gaps 10;

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QY 1 MRSKVALLIPALLAAGAAHAEVYKDKNKLIDYGVKDLHYFSDNKKVDGQDTYMRIG 60
  1 MKYKVLILVLPALLVAGAAHAEVYKDKNKLIDYGVKDLHYFSDNKKVDGQDTYMRIG 60
Db 1 MRSKVALLIPALLAAGAAHAEVYKDKNKLIDYGVKDLHYFSDNKKVDGQDTYMRIG 60
QY 61 FKGETVTOQLTGYGQWEOIQGNSAE--NENSWTRAFALCKQDVGSFPGYGRNYGVYD 119
  61 FKGETVTOQLTGYGQWEOIQGNSAE--NENSWTRAFALCKQDVGSFPGYGRNYGVYD 119
Db 61 FKGETVTOQLTGYGQWEOIQGNSAE--NENSWTRAFALCKQDVGSFPGYGRNYGVYD 119
QY 120 DVTSMVDLPEFGGDTY--GSDNFMQORNGFATYRNTDFEGLVDGLNFAVOYQGNKNGPS 178
  120 DVTSMVDLPEFGGDTY--GSDNFMQORNGFATYRNTDFEGLVDGLNFAVOYQGNKNGPS 178
Db 120 DVTSMVDLPEFGGDTY--GSDNFMQORNGFATYRNTDFEGLVDGLNFAVOYQGNKNGPS 178
QY 179 GEGFTSGV--TNNGRDALRONGDVGGSITYDY--ESFGISGAISSSKRTDAQ--NTAAYI 233
  179 GEGFTSGV--TNNGRDALRONGDVGGSITYDY--ESFGISGAISSSKRTDAQ--NTAAYI 233
Db 179 GEGFTSGV--TNNGRDALRONGDVGGSITYDY--ESFGISGAISSSKRTDAQ--NTAAYI 233
QY 234 GNDRAETTTGGLKYANNITYLAOYQOTYNATRVGSLGM--ANKRONEAVALQOFDEFG 291
  234 GNDRAETTTGGLKYANNITYLAOYQOTYNATRVGSLGM--ANKRONEAVALQOFDEFG 291
Db 234 GNDRAETTTGGLKYANNITYLAOYQOTYNATRVGSLGM--ANKRONEAVALQOFDEFG 291
QY 292 LRPSLAYLQSKGNL-----GRGYDEDLIKYVDVATYFNKMSYVDYKINLDD 343
  292 LRPSLAYLQSKGNL-----GRGYDEDLIKYVDVATYFNKMSYVDYKINLDD 343
Db 292 LRPSLAYLQSKGNL-----GRGYDEDLIKYVDVATYFNKMSYVDYKINLDD 343
QY 344 -DNQFTRDAGINTDNIYALGLVYQF 367
  344 -DNQFTRDAGINTDNIYALGLVYQF 367
Db 344 -DNQFTRDAGINTDNIYALGLVYQF 367
QY 353 EDDSFYAANGISPTDIALGLVYQF 377
  353 EDDSFYAANGISPTDIALGLVYQF 377
Db 353 EDDSFYAANGISPTDIALGLVYQF 377

```

## RESULT 3

US-09-041-889-28

Sequence 28, Application US/09041889

Patent No. 6033864

GENERAL INFORMATION:

APPLICANT: Braum, Jonathan

APPLICANT: Cohay, Offer

TITLE OF INVENTION: Diagnosis, Prevention and Treatment of

TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using

TITLE OF INVENTION: Microbial UC PANCA antigens

NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell &amp; Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/041,889

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/837,058

FILING DATE: 11-APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-PM 3006

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 323 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-09-041-889-28

Query Match 55.2%; Score 1078.5; DB 3; Length 323;  
 Best Local Similarity 66.2%; Pred. No. 1.5e-85;  
 Matches 219; Conservative 31; Mismatches 36; Indels 25; Gaps 9;

1 M K S K V I A L L I P A L L A A G A H A E V Y N K D G N K L D L G K Y D G L H F E S D N K D V D Q T Y M R L G 60  
 1 M K S K V I A L L I P A L L A A G A H A E V Y N K D G N K L D L G K Y D G L H F E S D N K D V D Q T Y M R L G 60  
 61 F K G E Q V T D L T G Y G M E Y O I G N S A F - N E N S W T R V A F A G L F O D V G S F D Y G R N Y G V Y 119  
 61 F K G E Q V T D L T G Y G M E Y O I G N S A F - N E N S W T R V A F A G L F O D V G S F D Y G R N Y G V Y 119  
 61 F K G E Q V T D L T G Y G M E Y O I G N S A F - N E N S W T R V A F A G L F O D V G S F D Y G R N Y G V Y 119  
 120 D V T S W T D V L P E R G S D T - G S D N F M O Q R G N F G A T Y R N T D F E G L V D G L N F A V O Y G K N G M P S 178  
 121 D I E G T M D I P E R G S D S Y T N A D N F M T G R A N G A T Y R N T D F E G L V D G L N F A V O Y G K N G M P S 176  
 179 G E G T S G V - T N N G R D A L R O N G D V G S I T Y D Y - E G F I G G A I S S S K R T D A Q - N T A A Y I 233  
 177 - E G A S N G E G T N N G R D V H E N G D G M G L S T Y D L G M G F S A G A Y T S S D R T N Q V N H T A A - 233  
 234 G N G D A E F Y T G L K D A N N I Y L A O Y T O T Y N A T R V G S L G W - A N A Q N F E A V A O Y Q E P F G 291  
 234 - G G D A D A M T A G L K Y D A N N I Y L A T M Y S E T R N M T P R G S D S D Y A V A N K T O N F E V T A G Y Q F D E G 292  
 292 L R P S L A V L O S K G N L - - - - - G R G Y D D E D 314  
 293 L R P A V S F L M S K G R D L H A A G A D N P A G V D K D 323

RESULT 4  
 US-08-355-844-1  
 Sequence 1, Application US/08355844  
 Patent No. 5940307

GENERAL INFORMATION:  
 APPLICANT: Fischbarg, Jorge  
 APPLICANT: Czegledy, Ferenc  
 APPLICANT: Iserovich, Pavel  
 APPLICANT: Li, Jun  
 APPLICANT: Cheung, Min  
 TITLE OF INVENTION: A METHOD FOR PREDICTING PROTEIN  
 TITLE OF INVENTION: STRUCTURE  
 NUMBER OF SEQUENCES: 3  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond  
 STREET: 30 Rockefeller Plaza  
 CITY: New York  
 STATE: NY  
 COUNTRY: USA  
 ZIP: 10112-0228  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/355,844  
 FILING DATE: 14-DEC-1994  
 CLASSIFICATION: 436  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Tang, Henry Y.S.  
 REGISTRATION NUMBER: 29,705  
 REFERENCE/DOCKET NUMBER: A29927-50/29910  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-408-2586  
 TELEFAX: 212-765-2519

INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 340 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 ORIGINAL SOURCE:  
 ORGANISM: Escherichia coli  
 FEATURE:  
 NAME/KEY: Peptide  
 LOCATION: 1..340  
 OTHER INFORMATION: OmpF porin protein  
 US-08-355-844-1

Query Match 52.6%; Score 1027; DB 2; Length 340;  
 Best Local Similarity 58.4%; Pred. No. 4.5e-81;  
 Matches 211; Conservative 45; Mismatches 69; Indels 36; Gaps 9;

22 A E V Y N K D G N K L D L G K Y D G L H F E S - - - - - D N K D V D Q T Y M R L G F K G E Q V T D L T G Y G O 76  
 1 A E I Y N K D G N K Y D L G K A V G L H R S K G N G E N S I G G N G D M T Y A R L G F K G E T Q I N S D L T G I G O 60  
 77 W E Y O I G N S A E N - - - E N N S W T R V A F A G L F O D V G S F D Y G R N Y G V Y D V T S W T D V L P E R G G 133  
 61 W E Y N Q G N N S E G A D A Q T O N K T R L A F A G L K Y A D V G S F D Y G R N Y G V Y D A L G T D M L P E R G G 120  
 134 D T Y G S D N F M O Q R G N F G A T Y R N T D F E G L V D G L N F A V O Y G K N G N S G E F T G C V T N N G D - 192  
 121 D T A V S D D F E V R G V G A T Y R N S N F E G L V D G L N F A V O Y L G K - - - - - N E R D T 165  
 193 A L R O N G D G V G S I T Y D Y G F I G G A I S S S K R T D Q N T A A Y I G N G R A T Y T G L K Y D A N N 252  
 166 A R R S N G D V G S I S T E R B G I V G A Y G A D R T N I D E - A Q I G N G K A Q O M T G L K Y D A N N 224  
 253 I Y L A A Y T O T Y N A T R V - - - - - G S L G M A N K A Q N F E A V A O Y Q E P F G L R P S L A V L O S K G N L G 307  
 225 I Y L A N Y G E T R N A P I T N K F T N T S G F A N K T O D V L L N A O Y Q F D G L R P S I A T T K S A K A Y - 283  
 308 R G Y D E D I L K Y D V G A T Y Y F N K N M S T Y V Y K I N L D - D N O F T R A G I N T D N I V A L G L Y Q 366  
 284 E G I G D V D L V N Y F E V G A T Y F N K N M S T Y V Y I I N O I S D N K L - - - - - G V G S D D T V A V G I Y Q 339  
 367 F 367  
 340 F 340

RESULT 5  
 PCT-US95-16126-1

Sequence 1, Application PC/WTUS9516126  
 GENERAL INFORMATION:  
 APPLICANT: Fischbarg, Jorge  
 APPLICANT: Czegledy, Ferenc  
 APPLICANT: Iserovich, Pavel  
 APPLICANT: Li, Jun  
 APPLICANT: Cheung, Min  
 TITLE OF INVENTION: A METHOD FOR PREDICTING PROTEIN  
 TITLE OF INVENTION: STRUCTURE  
 NUMBER OF SEQUENCES: 3  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond  
 STREET: 30 Rockefeller Plaza  
 CITY: New York  
 STATE: NY  
 COUNTRY: USA  
 ZIP: 10112-0228  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25

APPLICANT: Soper, Thomas S.



```

APPLICANT: Liang, Shu-Mei
TITLE OF INVENTION: A Method For The High Level
TITLE OF INVENTION: Expression,
TITLE OF INVENTION: Purification And Refolding Of The Outer Membrane
TITLE OF INVENTION: Protein
TITLE OF INVENTION: P2 From Haemophilus Influenzae Type b
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/08326
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096,181
FILING DATE: 23-JULY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REFERENCE/DOCKET NUMBER: 1438.001PC01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-08326-8

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Query Match      8.4%; Score 164.5; DB 5; Length 361;
Best Local Similarity 24.1%; Pred. No. 1.4e-06;
Matches 90; Conservative 52; Mismatches 145; Indels 87; Gaps 17;

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4 KVLALLPALLAAGAAAEVYNNKGLDLYGKVDLHFFSDKNDVDGQTY-----56
3 KITLALLVGAFAASAAANAAYVNNEGTNVELGRLSTIAEOS-NSTVDNOKOQHGALRNQ 61
57 -MRLGFKGETQVTDLTGYGOWEYQIOGNSAENENNSW---TRVAFGLKFDQVGSFDY 111
62 GSRPHIKATNHFQDGFYAQGYLFTRFYTKASENGSDNFGDITSKYAVVTLGKNAFGEVKL 121
112 GRNNGVYVDTSMVDLPEFGGDTYGSDFNFMQORGN-FGATIRRTDFFGLYVDGINFVQY 170
122 GRATYADGTTASD--KEG--VLNNSDYIPISGNTVGYTFKCID--GVLGANY-----171
171 QGKNGNSGEGFTSGVTNNGDALRONGDVGSGITVDYEGFCGALISSKRRDAQNTA 230
172 -----LLAQKREGAKG-----ENKRPNDKAGE 193
231 AYIG--NGRAETYTGLKYDANNIYLAQYTOT--YNATRVGSLGMANKAQ--NFEA 282
194 VRIGEINNIGIYV-----GAKYDANDIVAKIAYGRNTYKNYMSD-----EHKQQLNVLVA 242
283 VAQYQF-DGGLRPSLATLQSGKGLGSGYDDEDLIKLVVDGATYFNKNNSTYVDYKI--339
243 TLGFRFSDLGLVLSLQSGYAKTKNYKIKHEKR--YFVSPGFQYELMEDNIVYGNFKYER 299
340 NLDDNOFTRDAGI 353
300 TSVDOGEKTRQNAV 313

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RESULT 8
US-08-096-182A-4
Sequence 4, Application US/08096182A
Patent No. 543808
GENERAL INFORMATION:
APPLICANT: Blake, Milan S.
APPLICANT: Tai, Joseph Y.
APPLICANT: Qi, Hulin L.
APPLICANT: Liang, Shu-Mei
APPLICANT: Hronowski, Lucjan J.J.
TITLE OF INVENTION: Method for the High Level Expression,
TITLE OF INVENTION: Purification and Refolding of the Outer Membrane Group B
TITLE OF INVENTION: Porin Proteins from Neisseria Meningitidis
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Ave., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,182A
FILING DATE: 23-JUL-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1438.0060000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 342 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-096-182A-4

```

```

Query Match      7.2%; Score 140.5; DB 1; Length 342;
Best Local Similarity 25.6%; Pred. No. 0.00015;
Matches 81; Conservative 38; Mismatches 116; Indels 81; Gaps 21;

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58 RLGFKEGTQVTDLTGYGOWEYQIOGNSAENENNSW-TRVAFGLKFDQVGSFDYGR--N 114
43 KIFGKGEDLGNKKAIMOLE---QKASLAGTNSGWNROSFTGLK---GGGTYVAGN 95
115 YGVYV-----DYSMTVDLPEFGGDTYGSDFNFMQORNGFATYRNDFGL-----VDGL 164
96 LNTVLADSGGNVANW-----ESSGNT-----EDVGLGTTGRVESR 131
165 NFAVQYQKNGNPSGEGFTSGV---TNNGRDA-----LRONGDVGGSITVDYEGFGIG 215
132 EISVRD-----SPVAFGSSGTYVPRDANDVDKYKTKSRESYHAGLKYENAGFGQ 187
216 GAISSSK-----RTDAQNTAAYTNGDRAETV-----TGGLKYANNIY--LAQYTOTYN 264
188 YASFQKAYADLNTDAERVAANTANAPRVKDYVHRVYAG--YDANDLYVSVAQGYEAKN 245
265 ATRVAGSL-GWANKAONFEAAYQYDFGLRPSLAYLOS--KGKMLG--RGYDDEDILKYV 319
246 -NEVGSTKGGKKHQTQYAAATAATRFQ-NYTPRVSYAHGKRAKYNGKANDAYQYDQYI---300
320 DVGATYYFNKNNSTYV 335

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Db 301 -VGADYDFSKRTSALY 315

## RESULT 9

US-08-877-109-4  
Sequence 4, Application US/08877109  
Patent No. 5747287

## GENERAL INFORMATION:

APPLICANT: Blake, Milan S.  
APPLICANT: Tai, Joseph Y.  
APPLICANT: Qi, Hulin L.  
APPLICANT: Liang, Shu-Mei  
APPLICANT: Hronowski, Lucjan J.J.  
APPLICANT: Pullen, Jeffrey K.  
TITLE OF INVENTION: Method for the High Level Expression,  
TITLE OF INVENTION: Purification and Refolding of the Outer Membrane Group B  
TITLE OF INVENTION: Purin Proteins from Neisseria meningitidis  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Ave., NW  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/877,109  
FILING DATE:

## CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/431,264

FILING DATE: 28-APR-1995

APPLICATION NUMBER: 08/096,182

FILING DATE: 23-JUL-1993

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 1438.0060001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 342 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-877-109-4

Query Match 7.2%; Score 140.5; DB 1; Length 342;

Best Local Similarity 25.6%; Pred. No. 0.00015;

Matches 81; Conservative 38; Mismatches 116; Indels 81; Gaps 21;

Query Match 7.2%; Score 140.5; DB 3; Length 342;

Best Local Similarity 25.6%; Pred. No. 0.00015;

Matches 81; Conservative 38; Mismatches 116; Indels 81; Gaps 21;

Db 188 YAGSFAYADLNTDAERVAANTANAHVVDYQVHRVAG--YDANDLYSVAGQYBAKN 245  
QY 265 ATRVGSU-GWANKAQNENEAQOYDFGLRSLAYLOS--KGNLGS--RGYDEDILTKY 319  
Db 246 -NEVGSTGKKHEOTOVAALAAVYRFG-NVTPRVSAHGFRKAVGYKDAYTQDYI--- 300  
QY 320 DVGATYFENKMSYV 335  
Db 301 -VGADYDFSKRTSALY 315

## RESULT 10

US-08-798-760-4  
Sequence 4, Application US/08798760  
Patent No. 6013267

## GENERAL INFORMATION:

APPLICANT: Blake, Milan S.  
APPLICANT: Tai, Joseph Y.  
APPLICANT: Qi, Hulin L.  
APPLICANT: Liang, Shu-Mei  
APPLICANT: Hronowski, Lucjan J.J.  
APPLICANT: Pullen, Jeffrey K.  
TITLE OF INVENTION: Method for the High Level Expression,  
TITLE OF INVENTION: Purification and Refolding of the Outer Membrane Group B  
TITLE OF INVENTION: Purin Proteins from Neisseria Meningitidis  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Ave., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/798,760  
FILING DATE: 11-FEB-1997

## CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 1438.0060002

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 342 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-798-760-4

Query Match 7.2%; Score 140.5; DB 3; Length 342;

Best Local Similarity 25.6%; Pred. No. 0.00015;

Matches 81; Conservative 38; Mismatches 116; Indels 81; Gaps 21;

QY 58 RLKFGKGTQVTDLTGIGMEYIOGNSAENENNSW-TRVAFGLKFOVGSFYGR--N 114  
Db 43 KIFKQEDIGNMKAIMOLE--OKASITAGTNSGNGNOSFGLK---GGFGYVRA 95  
QY 115 YGVVY---DVTSMVDVLPFEGGDTYGSDFNQGRNGFATYRNTDFGL-----VDGL 164  
Db 96 LNTVLDSGDNVAVM-----EGSNT-----EDVLGLTIGRVER 131  
QY 165 NFAVVOYQKNGNPSGEGFTSGV---TNNGRDA---LRONGDVGGSTIYDEFGIG 215  
Db 132 EISVRD---SVPFAGFSSGVYVPRDNANDVDKTKHTKSSRESYHAGIKYENAGFGQ 187  
QY 216 GAISSK---RTDAONTAAYIGNGRATY---TGILKDYANNIY---LAAQYOTY 264

Db 132 EISRYD-----SPVFAGSGSVQYVPPRDNANDVKYKHTSSRSRYHAGLKYENAGFFGQ 187  
QY 216 GAISSSK-----RTDAQNTAAYIGNGDRAETV-----TGLKYDANNIY--LAAQYQTQYN 264  
Db 188 YAGSFAYADLNTDAEVAAYNTANAHFYKDYQYHRYVAG--YDANDLYVYAGQYEAKN 245  
QY 265 ATRVGSU-GMANKAONEEVAAYOFDFGLRPSLAYLOS-KGNLIG---RGYDEDEDILKYV 319  
Db 246 -NEVGSYFKKKHEDQTYAATAAYRFG-NVTPRVSYAHGFAYKNGVANDANYQYDQYI--- 300  
QY 320 DVGATYYFNKMMSTYV 335  
Db 301 -VGADYDFSKRTSALV 315

## RESULT 11

PCT-US94-08327-4  
Sequence 4, Application PC/TUS9408327  
GENERAL INFORMATION:  
APPLICANT: The Rockefeller University  
APPLICANT: 1230 York Avenue  
APPLICANT: New York, New York 10021  
APPLICANT: United States of America  
APPLICANT: 12103 Indian Creek Court  
APPLICANT: Beltsville, Maryland 20705  
APPLICANT: United States of America  
APPLICANT: Tai, Joseph Y.  
APPLICANT: Qi, Hulin L.  
APPLICANT: Liang, Shu-Mei  
APPLICANT: Hronowski, Lucjan J.J.  
APPLICANT: Pullen, Jeffrey K.  
TITLE OF INVENTION: Method for the High Level  
TITLE OF INVENTION: Expression,  
TITLE OF INVENTION: Purification and Refolding of the Outer Membrane  
TITLE OF INVENTION: Group B  
TITLE OF INVENTION: Porin Proteins from Neisseria Meningitidis  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Ave., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/08327  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/096,182  
FILING DATE: 23 July 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1438.006PC00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 342 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US94-08327-4

Query Match 7.28; Score 140.5; DB 5; Length 342;

Best Local Similarity 25.6%; Pred. No. 0.00015;  
Matches 81; Conservative 38; Mismatches 116; Indels 81; Gaps 21;

QY 58 RLGFKEGTQYDOLTGCGMEYQIOGSANENNSW--TRVAFGLKRPQDGSFQYGR--N 114  
Db 43 KIGFKGEGDLNGKMAKATQLE-----QKASIACTNSGKWNRSFGLK-----GGCTYAGN 95  
QY 115 YGVVY-----DYSWTDVLEPFEGDITYGSDNFMQRCNFGATYRNDFGL-----VDGL 164  
Db 96 LNFVLKDSGDNVNAM-----ESGSNT-----EDVLIGTIGVRESR 131  
QY 165 NFAVQYQKKNNGPSGEFTSGV-----TNGRDA-----LQNGDGVGSGSTIYEGGIG 215  
Db 132 EISRYD-----SPVFAGSGSVQYVPPRDNANDVKYKHTSSRSRYHAGLKYENAGFFGQ 187  
QY 216 GAISSSK-----RTDAQNTAAYIGNGDRAETV-----TGLKYDANNIY--LAAQYQTQYN 264  
Db 188 YAGSFAYADLNTDAEVAAYNTANAHFYKDYQYHRYVAG--YDANDLYVYAGQYEAKN 245  
QY 265 ATRVGSU-GMANKAONEEVAAYOFDFGLRPSLAYLOS-KGNLIG---RGYDEDEDILKYV 319  
Db 246 -NEVGSYFKKKHEDQTYAATAAYRFG-NVTPRVSYAHGFAYKNGVANDANYQYDQYI--- 300  
QY 320 DVGATYYFNKMMSTYV 335  
Db 301 -VGADYDFSKRTSALV 315

## RESULT 12

US-08-096-182A-6  
Sequence 6, Application US/08096182A  
Patent No. 5439808  
GENERAL INFORMATION:  
APPLICANT: Blake, Milan S.  
APPLICANT: Tai, Joseph Y.  
APPLICANT: Qi, Hulin L.  
APPLICANT: Liang, Shu-Mei  
APPLICANT: Hronowski, Lucjan J.J.  
APPLICANT: Pullen, Jeffrey K.  
TITLE OF INVENTION: Method for the High Level Expression,  
TITLE OF INVENTION: Purification and Refolding of the Outer Membrane Group B  
TITLE OF INVENTION: Porin Proteins from Neisseria Meningitidis  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Ave., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/096,182A  
FILING DATE: 23-JUL-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1438.0060000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 363 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-096-182A-6



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: REFERENCE/DOCKET NUMBER: 1438. 0060002
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 371-2600
: TELEFAX: (202) 371-2540
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 363 amino acids
:   TYPE: amino acid
:   TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-798-760-6
:
: Query Match      7.2%  Score 140.5;  DB 3;  Length 363;
: Best Local Similarity 25.6%;  Pred. No. 0.00016;
: Matches 81;  Conservative 38;  Mismatches 116;  Indels 81;  Gaps 21.
:
: QY  58  RLGFGEHQVYDQLTGYQWQVEYQIQGNSAENNNNSW-TRVAAGLKFQVDSFDDGR--N 114
:      ::||||: : : : : | | | | : : : : | | | | | | | | | | | | | | | |
: Db   64  KIGFGEQEDLNGMAIMOLE---OKASITAGTNSGNGRQSTIGLK---GGFTVRAGN 116
:      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
: QY  115  YGVVY-----DVTGWTVDLPFGGDTYSDDNMQRCNFGATYRMTDFGL-----VDGL 164
:      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
: Db   117  LNTVLYGSGDVVNM-----ESGNT-----EDVIGLGTIGRVER 152
:      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
: QY  165  NFAVOYQKNGNPSGEGFTSGV---TNGGRDA-----LRONGDVGGSITYDYEGFGIG 215
:      : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
: Db   153  EISVRD---SPVFAGSGSVQYVPRDNANDVDKXHTKSSRESYHAGLKYEANGFFQO 208
:      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
: QY  216  GAISRSK-----RTDQNTAAIYIGNDRLETY-----TGCLKDANNIY--LAAQTQTQTN 264
:      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
: Db   209  YAGSPAKYADLNTLAEKRAVNTANHPVKDYQVHRVVG--VDANDLYVSAGVGEAAKN 266
:      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
: QY  265  ATRVGSIL-GMANKQNFPAVAVOCPDFGLRPLAYLOS-KGKNLGG---RGYDEDELTKYV 319
:      || | : : | : | : | : | : | : | : | : | : | : | : | : | : |
: Db   267  -NEVGSTGKKHEDQTVAATAIRRG-NVTPRVSTAHGFKAKVNGVKANTQYDYI--- 321
:      || | : : | : | : | : | : | : | : | : | : | : | : | : | : |
: QY  320  DVGATYYENKKNMSTYV 335
:      || | | | | | | | |
: Db   322  -VGADYDFSKRTSALV 336
:
: RESULT 15
: PCT-US94-08327-6
: Sequence 6, Application PC/TUS9408327
: GENERAL INFORMATION:
: APPLICANT: The Rockefeller University
: APPLICANT: 1230 York Avenue
: APPLICANT: New York, New York 10021
: APPLICANT: United States of America
: APPLICANT: 12103 Indian Creek Court
: APPLICANT: Beltsville, Maryland 20705
: APPLICANT: United States of America
: APPLICANT: Tai, Joseph Y.
: APPLICANT: Qi, HuiLin L.
: APPLICANT: Liang, Shu-Mei
: APPLICANT: Hironowski, Lucjan J.J.
: APPLICANT: Pullen, Jeffrey K.
: TITLE OF INVENTION: Method for the High Level
: TITLE OF INVENTION: Expression,
: TITLE OF INVENTION: Purification and Refolding of the Outer Membrane
: TITLE OF INVENTION: Group B
: TITLE OF INVENTION: Porin Proteins from Neisseria Meningitidis
: NUMBER OF SEQUENCES: 23
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Sterne, Kessler, Goldstein & Fox
: STREET: 1100 New York Ave., Suite 600
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20005-3934
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk

```

```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/08327
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 23 July 1993
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1438, 006PC00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 363 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-08327-6

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Query Match	7.2%	Score	140.5	DB	5	Length	363	
Best Local Similarity	25.6%	Pred.	No. 0.00016					
Matches	81	Conservative	38	Mismatches	116	Indels	81	Gaps
								21.
QY	58	RLRGKETQVTDLTGCGWGEYQLOGNSAENENNSW-TRVAFAGLKFDQVGSFEDYGR--N	114					
		:						
Db	64	KIGRGGQDLDLNGKMAIMQLE---QKASIAGTNSGWRQSPHIGLK-----GGFGTVRAGN	116					
QY	115	YGVVY-----DYTSKTDVLPFEGGDPTYSDDNFMQQRGNFGATYRTDFFGL-----VDGL	164					
		:						
Db	117	LNTFLKDSGDVNVNVA-----EGSNT-----EDVLGLETIGRVESR	152					
QY	165	NFAVOYQKKNPNPSEGEFTSGV-----TNNGRDA-----LRQNGDGVGSITPYDYGFGIG	215					
		:						
Db	153	EISVRYD---SPVPAGSGSVQVYPRGNANDVDKTKTKSSRESYHAAGLKEYENAGFFGQ	208					
QY	216	GAISSSK-----RTQAQNTAAIYIGNDRAETV-----TGGLKYDANNIY--LAAQYTOTVN	264					
		:						
Db	209	YAGSEFAKADLNTDAERAAYVTAHNPVKDYQVHRVYAG--YDANDLYVSAGQVEAANKN	266					
QY	265	ATRVGSL-GWANKAKNFEAFAVAQYQDFGLRSLAYLAGS-KGKNILG---RGYDDEDILKYV	319					
		:						
Db	267	-NEVSGTSGKKHEQIQVAVATAAAYRFG-NVTPRVSYAHGFFAKKAVNGVKDANYQDOVI---	321					
QY	320	DVGATYYFNKNMSTVY	335					
		:						
Db	322	-VGADYDFSKRTSALV	336					

Search completed: August 21, 2001, 20:58:50  
Job time: 65 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 21, 2001, 20:57:40 ; Search time 20.32 Seconds  
(without alignments)  
1094.931 Million cell updates/sec

Title: US-09-575-061-1  
Perfect score: 1953  
Sequence: 1 MKSKYLLALLIPALLAAGAAH.....TRDAGINTDNLVALGLVYQF 367

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues  
Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

A\_Geneseq\_0601:\*

1:	/SID8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
2:	/SID8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
3:	/SID8/gcgdata/geneseq/geneseqp/AA1982.DAT:*
4:	/SID8/gcgdata/geneseq/geneseqp/AA1983.DAT:*
5:	/SID8/gcgdata/geneseq/geneseqp/AA1984.DAT:*
6:	/SID8/gcgdata/geneseq/geneseqp/AA1985.DAT:*
7:	/SID8/gcgdata/geneseq/geneseqp/AA1986.DAT:*
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9:	/SID8/gcgdata/geneseq/geneseqp/AA1988.DAT:*
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21:	/SID8/gcgdata/geneseq/geneseqp/AA2000.DAT:*
22:	/SID8/gcgdata/geneseq/geneseqp/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1914	98.0	367	20	AAV42549
2	1914	98.0	367	20	AAV34058
3	1914	98.0	367	21	AAV57356
4	1285	65.8	377	20	AAV34057
5	1285	65.8	377	21	AAV57355
6	1104	56.5	362	20	AAV42550
7	1078.5	55.2	323	20	AAV34056
8	1078.5	55.2	323	21	AAV57354
9	1027	52.6	340	17	AAW92998
10	226.5	11.6	89	18	AAW27781
11	187.5	9.6	353	20	AAV26025
					OMP protein of H.

12	176	9.0	362	10	AAW90098	P2 antigen of Haem
13	174	8.9	343	20	AAV26024	OMP protein of Pa
14	171	8.8	353	20	AAV26023	OMP protein of Pa
15	164.5	8.4	361	11	AAW05999	P2 gene product of
16	164.5	8.4	361	16	AAW68877	H. influenzae p2 e
17	161.5	8.3	350	18	AAW21678	Haemophilus influe
18	148.5	7.6	350	13	AAW27484	protein IB. Synth
19	147.5	7.6	350	10	AAW90100	Class II outer mem
20	146	7.5	353	11	AAW60308	Gonococcal porin-5
21	145.5	7.5	372	16	AAW60607	Mature class 2 por
22	140.5	7.2	342	16	AAW70763	Neisseria meningit
23	140.5	7.2	342	18	AAW21742	Fusion Class 2 por
24	140.5	7.2	363	16	AAW70764	Neisseria meningit
25	140.5	7.2	363	18	AAW21743	Class IB outer mem
26	132	6.8	328	11	AAW60306	P3 gene product of
27	130.5	6.7	341	11	AAW07043	A surface protein
28	128.5	6.6	589	20	AAW23745	Class IA outer mem
29	127.5	6.5	326	11	AAW06037	Class I OMP derive
30	127.5	6.5	363	16	AAW68878	Class I OMP derive
31	127.5	6.5	373	11	AAW06043	Class I OMP derive
32	126.5	6.5	342	16	AAW68879	H. influenzae prot
33	126.5	6.5	342	16	AAW68880	Class I OMP derive
34	126.5	6.5	366	11	AAW06044	Meningococcal Pl.7
35	125.5	6.4	373	14	AAW37328	Class I OMP derive
36	125	6.4	368	11	AAW06042	Class I OMP derive
37	124.5	6.4	341	11	AAW07042	P3 gene product of
38	124.5	6.4	511	17	AAW95012	C. difficile toxin
39	124.5	6.4	511	17	AAW95371	C. difficile toxin
40	124.5	6.4	608	17	AAW95013	C. difficile toxin
41	124.5	6.4	609	17	AAW95018	C. difficile toxin
42	124.5	6.4	611	17	AAW95372	C. difficile toxin
43	124.5	6.4	2366	17	AAW95011	Clostridium diffic
44	124.5	6.4	2366	19	AAW68388	Class I outer memb
45	121	6.2	373	11	AAW06035	

#### ALIGNMENTS

RESULT 1		
AAV42549	standard; Protein; 367 AA.	
AC	AAV42549;	
DT	20-DEC-1999 (first entry)	
DE	E. coli wild-type ompc protein.	
KW	Bacteria: attenuation; deletion; mutant; vaccine; immune response;	
KW	Gram negative; infection; diarrhoea; food poisoning; typhoid;	
KW	salmonellosis; gonorrhoea; gastroenteritis; whooping cough.	
OS	Escherichia coli.	
XX		
PN	W09949026-A1.	
XX		
PD	30-SEP-1999.	
XX		
PF	25-MAR-1999; 99WO-GB00935.	
XX		
PR	25-MAR-1998; 98GB-0006449.	
XX		
PA	(PEPT-) PEPTIDE THERAPEUTICS LTD.	
XX		
PI	Chalfield SN;	
XX		
DR	WPI: 1999-580447/49.	
XX		
DR	N-PSDB; AA222885.	
XX		
PT	New attenuated bacteria useful as vaccines for protecting against	
XX	infections	







**SQ Sequence 377 AA;**

CC This sequence represents the *E. coli* wild-type ompF protein. The coding  
CC sequence of the ompF gene was removed via PCR using primers TT1-TT4  
CC

CC (AA22889-222893) to produce a non-reverting deletion mutation. The  
 CC mutant ompF gene (AA222888) was used in the production of a bacterium  
 CC attenuated by a non-reverting mutation in each of the ompF gene, the arcC  
 CC gene (AA222883, AA222884), and the ompC gene (AA222885, AA222886). The  
 CC mutant bacteria provide immunogenic activity with reduced virulence and  
 CC thus can be used as a vaccine for raising an immune response against a  
 CC variety of bacteria in a mammalian host. Such vaccines can provide  
 CC protection against e.g., E. coli (a cause of diarrhoea in humans),  
 CC *Salmonella typhimurium* (the cause of salmonellosis in several animal  
 CC species), *S. typhi* (the cause of human typhoid), *S. enteritidis* (a cause  
 CC of food poisoning in humans), *S. choleraesuis* (a cause of salmonellosis  
 CC in pigs), *S. dublin* (a cause of both a systemic and diarrhoeal disease in  
 CC cattle, especially of new-born calves), *Haemophilus influenzae* (a cause  
 CC of meningitis), *Neisseria gonorrhoeae* (a cause of gonorrhoea), *Yersinia*  
 CC *enterocolitica* (the cause of a spectrum of disease in humans ranging  
 CC from gastroenteritis to fatal septicemic disease), *Bordetella pertussis*  
 CC (the cause of whooping cough), and *Brucella abortus* (a cause of abortion  
 CC and infertility in cattle and a condition known as undulant fever in  
 CC humans).

Sequence 362 AA:

Query Match 56.5%; Score 1104; DB 20; Length 362;  
 Best Local Similarity 58.9%; Pred. No. 1.3e-80;  
 Matches 225; Conservative 49; Mismatches 72; Indels 36; Gaps 9;

1 M K S V I A L L P A L L A G A A H A E Y N K D G N K L D Y G V D L G L H F S D N K D V D G D Q T Y M R L G 55  
 2 M K N I L A V P A L L V A G T A A A E Y N K D G N K L D Y G K A V L H Y F S K G N G E N S Y G G N G D M T 61  
 56 Y M R L G K E T O V D L T G Y G O M E Y O L O G N S A E N E N N S M T R A F A G L K F O D V G S F D Y G 112  
 62 Y A R L G F G E Q I N S D L T G Y G Q W E Y N F G N S E G A D Q T G K T L A F G L K Y A D W G S T D Y G 121  
 113 R N T G V Y D V T S W T D V L P E F G S D T Y G S D N F M Q R G N F G A T Y R N T D F G L V D G L N F A V O Y G 172  
 122 R N G V Y V D A L G Y C M L P E F G S D T Y G S D F F V R Y G V A T Y R N S F F G L V G L N F A V G Y L G 181  
 173 K N G P S E G T S G V T N N G R P A L R Q N D G Y G S T T Y B E F G I G A I S S K R D A Q M T A A 231  
 182 K -----N E T L A R T N S G D V G S I S Y E G F I G Y A G A A D R T L I G E A Q 225  
 232 Y I G N D R A E T Y T G L K Y D A N N I Y L A A Q T Y T Y N A T R V -----G S I G W A N K A Q N F E A V A Q Y 286  
 226 P L G N G K A E G W A G L K Y D A N N I Y L A A Y G E T R A T P L N T F N T S G F A N K T Q D V L I Y A G Y 285  
 287 Q P D F G L R P S L A Y L O S K G N L G R G Y D E D I L K Y D V G A T Y Y F N K N M S T Y V D K I N L D - D N 345  
 286 G F D G I R P S I A Y L E T S K A K A V - E G I G D V D L V N Y F E V A G A T Y Y F N K M S T Y V D I L N Q I A S D N 344  
 346 Q F T R D A G I N D N T V A L G Y A Q F 367  
 345 K L -----G V G S D D T V A V G I Y G F 362

RESULT 7

ID AAY34056 standard; protein; 323 AA.

AC AAY34056;

23-NOV-1999 (first entry)

E. coli outer membrane protein F precursor.

ulcerative colitis; histone; H1-like antigen; porin antigen;  
 Bacteroides antigen; IBD; PANCA; inflammatory bowel disease;  
 diagnosis; perinuclear anti-neutrophil cytoplasmic antibody;  
 outer membrane protein F precursor.

Escherichia coli.

PN W09455955-A1.

XX 16-SEP-1999.

PF 12-MAR-1999; 99NO-US05492.

PR 12-MAR-1998; 98US-0041889.

PA (REGC ) UNIV CALIFORNIA.

PI Braun J, Cohavy O;

DR WPI; 1999-551215/46.

PT Use of histone H1, porin or Bacteroides antigens as targets for the

PT diagnosis, prevention and treatment of ulcerative colitis

PS Claim 8; Fig 11; 134pp; English.

XX The invention provides a method for the diagnosis, prevention and  
 CC treatment of ulcerative colitis (UC) using histone H1-like antigen, a  
 CC porin antigen or a Bacteroides antigen as a target antigen. The novel  
 CC method of diagnosing UC in a subject suspected of having inflammatory  
 CC bowel disease (IBD) comprises: (1) obtaining a sample from the subject;  
 CC (2) contacting the sample with a histone H1-like antigen, or perinuclear  
 CC anti-neutrophil cytoplasmic antibody (PANCA)-reactive fragment, to form a  
 CC complex of the histone H1-like antigen, or the PANCA-reactive fragment,  
 CC and antibody to the histone H1-like antigen; and (3) detecting the  
 CC presence or absence of the complex, where the presence of the complex  
 CC indicates that the subject has UC. The PANCA-reactive histone H1-like  
 CC antigen, porin antigen and Bacteroides antigen are useful in the  
 CC diagnosis, prevention and treatment of UC. The methods can also be used  
 CC for identifying agents useful for treating UC. The present sequence  
 XX represents a E. coli outer membrane protein F precursor.

Sequence 323 AA:

Query Match 55.2%; Score 1078.5; DB 20; Length 323;  
 Best Local Similarity 66.2%; Pred. No. 1.2e-78;  
 Matches 219; Conservative 31; Mismatches 56; Indels 25; Gaps 9;

1 M K S V I A L L P A L L A G A A H A E Y N K D G N K L D Y G V D L G L H F S D N K D V D G D Q T Y M R L G 60  
 1 M K E V I A L L P A L L A G A A H A E Y N K D G N K L D Y G K A V L H Y F S D N S A K D G S Y A R L G 60  
 61 F K G E T O V T D L T G Y G O M E Y O I Q N S A E N E N N S M T R A F A G L K F O D V G S F D Y G A N T V Y 119  
 61 F K G E T I N D L T G Y G Q W E Y N I G A N T E S S K N G S W T R I A F A G L K Y A D W G S T D Y G R N Y G M Y 120  
 120 D V T S W T D V L P E F G S D T Y - G S D N F M Q R G N F G A T Y R N T D F G L V D G L N F A V O Y G K N N P S 178  
 121 D I E G W C M L P E F G S D T Y N A D N I M T G R A N G V A T Y R N D F I G L V N G L N F A V G Y G N M ----- 176  
 179 G E G F T S G V - T N N G R D A L R O N G D G V G S I T Y D Y - E G F I G A I S S S K R T A Q - N T A Y I 233  
 177 - E G A S N G Q E G T N G R D R H E N G D G W J S T L Y D I G M F S G A A Y T S S D R T N D Y N H T A A - 233  
 234 G N G D R A E T Y T G L K Y D A N N I Y L A A Q T Y T Y N A T R V G S L G W - A N K A Q N F E A V A Q Y O P D F G 291  
 234 - G G D K A D A W T A G L K Y D A N N I Y L A T M Y S E T R N M L P F G S D Y A V A N K I G N F E V T A G Y Q I D F G 292  
 292 L R P S L A Y L O S K G N L -----G R G Y D D D 314  
 293 L R P A V S T I M S K Y R D L H A A G A D A N P A G V D K D 323

RESULT 8

ID AAY57354 standard; protein; 323 AA.

AC AAY57354;

```

DT 13-JUN-2000 (first entry)
XX
DE E. coli outer membrane protein F precursor.
XX
KM ulcerative colitis; inflammatory bowel disease; porin antigen; MAb;
XX PANCA; perinuclear anti-neutrophil cytoplasmic antibody;
XX histone H1; outer membrane protein F precursor.
XX
OS Escherichia coli.
XX
PN US6033864-A.
XX
PD 07-MAR-2000.
XX
PF 12-MAR-1998; 98US-0041889.
XX
PR 12-APR-1996; 96US-0057846.
XX 11-APR-1997; 97US-0837058.
XX (REGC ) UNIV CALIFORNIA.
XX
PI Cohavy O, Braun J;
XX
DR MPI; 2000-255695/22.
XX
PT Diagnosing ulcerative colitis or susceptibility, by detecting complex
PT formation between microbial porin antigen and perinuclear
PT anti-neutrophil cytoplasmic autoantibodies -
XX
PS Claim 1; Fig 10; 49pp; English.
XX
CC The invention provides a method for diagnosing ulcerative colitis in a
CC subject suspected of having inflammatory bowel disease. The method
CC comprises reacting a patient sample with a porin antigen that is
CC immunologically reactive with PANCA (perinuclear anti-neutrophil
CC cytoplasmic antibodies) and detecting formation of a Ag-PANCA complex
CC as indicative of ulcerative colitis. The method is used to diagnose
CC ulcerative colitis or susceptibility to it. The present sequence
CC represents a E. coli outer membrane protein F precursor.
XX
XX Sequence 323 AA:

Query Match 55.2%; Score 1078.5; DB 21; Length 323;
Best Local Similarity 66.2%; Pred. No. 1.2e-78;
Matches 219; Conservative 31; Mismatches 56; Indels 25; Gaps 9;

QY 1 MRSKVIALIPALLAAGAAHAEVYKDGKLDLYGKVDGLHFSDKDVGQOTWRIG 60
DB 1 mskkviallilpallaagaaevykdgnklilygvdlhlyfsdksakdgdsyarlg 60
QY 61 FKRETOVTDLTGYGOMEVYIOGNSAE--NENNSMTRYAFAGLFEODVGSFDRNGYVY 119
DB 61 fkretovtldltgygomevniognsaenennsmtrvafaglfepodvgsfdrngyvvy 119
QY 120 DVTSMTDVLPEFGDLY--GSDNFMQORGNFGATRYNTDFEGLVDGLNFAVOYOGKNGNPS 178
DB 120 dvtsmtdvlpfegfdly--gsdnfmqorgnfgatryntdfeglvdglnfavoogkngnps 178
QY 121 diegwtdmpefsgdsytlnadnfmtrangvatyrntdfgylnglnfavqygnm---- 176
DB 121 diegwtdmpefsgdsytlnadnfmtrangvatyrntdfgylnglnfavqygnm---- 176
QY 179 GEGFTISGV--TNNGRDALRONGDVGGSITYYD--EGFGIGAISSSKRIDAQ--NTAAYT 233
DB 179 gegftisgv--tnngrdalrongdvggsityyd--egfgigaiSSSKRIDAQ--ntaayt 233
QY 234 GNGDRAEYTGIGKYDANNIYLAOYTOTRYNATRVGSLG--ANKQNEFAVAOYQEDFG 291
DB 234 gngdraeytgigkydanniylaoytotrynatrvgsLg--ankqnefaVAOYQEDFG 291
QY 292 LRPSLAYLQSKGKNL-----GRGYDDED 314
DB 292 lrpsvflmskgkrdlnaaggadnpgavddk 323

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AAW92998
ID AAW92998 standard; protein; 340 AA.
XX
AC AAW92998;
XX
DT 19-MAY-1999 (first entry)
XX
DE E. coli OmpF porin protein.
XX
KM OmpF; porin; amphiphilic alpha-structure; beta-structure; GLUT;
XX membrane protein; glucose transporter protein; function.
XX
OS Escherichia coli.
XX
PN WO9618957-A1.
XX
PD 20-JUN-1996.
XX
PF 13-DEC-1995; 95WO-US16126.
XX 14-DEC-1994; 94US-0355844.
XX (UYCO ) UNIV COLUMBIA NEW YORK.
XX
PI Cheung M, Czegledy F, Fischbarg J, Iserovich P;
XX IJ J;
XX
DR MPI; 1996-300839/30.
XX
PT Predicting tendency to form amphiphilic alpha and beta structures -
PT using a novel algorithm to calculate values for subsequent graphical
PT analysis to predict protein structure
XX
PS Disclosure; Fig 2; 106pp; English.
XX
CC This invention describes a novel method for predicting the tendency of
CC a protein to form either: (a) an amphiphilic alpha-structure or (b) an
CC amphiphilic beta-structure. The methods are used particularly for
CC predicting the structure of membrane proteins such as glucose transporter
CC proteins (GLUTs). They can be used to discern the function of proteins.
CC They can also be used for the rational design or identification of
CC compounds which interact with the proteins or to engineer proteins having
CC particular structures. This sequence represents an Escherichia coli
CC OmpF porin which is used to illustrate the method of the invention.
XX
XX Sequence 340 AA:

Query Match 52.6%; Score 1027; DB-17; Length 340;
Best Local Similarity 58.4%; Pred. No. 1.8e-74;
Matches 211; Conservative 45; Mismatches 69; Indels 36; Gaps 9;

QY 22 AEVYKNDGKRLDLYGKVDGLHFS-----DNKVDGDQTYMRGFGGEQVTDQLTGYGQ 76
DB 22 aeivyknDGKRLDLYGKVDGLHFS-----dnkvdgdqTYMRGFGGEQVTDQLTGYGQ 76
QY 77 WEQIOGNSAEN---ENNSMTRVAFAGLFEODVGSFDRNGYVYDVTSMTDVLPEFG 133
DB 77 weqioGNSAEN---ennsMTRVAFAGLFEODVGSFDRNGYVYDVTSMTDVLPEFG 133
QY 141 WEYNFGNMSGAGDAGTGNLTIRIAFAGLYADVGSIDYGRNYYVYDALGYTDMPEFG 120
DB 141 weynfgnMSGAGDAGTGNLTIRIAFAGLYADVGSIDYGRNYYVYDALGYTDMPEFG 120
QY 134 DRYGSDNFMQORGNFGATRYNTDFEGLVDGLNFAVOYOGKNGNPSGEGFTSGVTNNGRD- 192
DB 134 drygsdnfmqorgnfgatryntdfeglvdglnfavoogkngnpsGEGFTSGVTNNGRD- 192
QY 121 dtaysdfffvgrvgvatyrnsnffglvgdlnfavgyLg-----nerdt 165
DB 121 dtaysdfffvgrvgvatyrnsnffglvgdlnfavgyLg-----nerdt 165
QY 193 ALRQNDGCVGGSITYYEGFGIGAISSSKRIDAQNTAAYINGDGAETTYTGSLKTDANN 252
DB 193 alrQNDGCVGGSITYYEGFGIGAISSSKRIDAQNTAAYINGDGAETTYTGSLKTDANN 252
QY 166 arrnsdgyvgsisyebyfglyvgyaadtlnlge-aaplgnqkkaeqwaqglkydanm 224
DB 166 arrnsdgyvgsisyebyfglyvgyaadtlnlge-aaplgnqkkaeqwaqglkydanm 224
QY 253 IYLAOYTOTRYNATRV-----GSLGWANKRQNEFAVAOYQEDFGLRPSLAYLQSKGKNL 307
DB 253 iylaoytotrynatrv-----gslGWANKRQNEFAVAOYQEDFGLRPSLAYLQSKGKNL 307
QY 225 iylaanygetmatpiltntfntsgfanktdvllvaqyqfdgtrpslaylkskxkv- 283
DB 225 iylaanygetmatpiltntfntsgfanktdvllvaqyqfdgtrpslaylkskxkv- 283
QY 308 RGYDDEDILKYVDVATYFNKNMSTYVDYKINLAD--DNOFTRDAGINTDNIVALGLVYQ 366

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Db	egigldvnyfeygatryfkmstvyvdylingidsnkl-----gygsddtravgylyq	339
Oy	367 F 367	
Db	340 F 340	
RESULT	10	
ID	AAW27781	
XX	AAW27781 standard; Protein: 89 AA.	
XX	AAW27781;	
DT	21-JUL-1998 (first entry)	
DE	Amino acid sequence of an outer membrane protein F precursor.	
XX		
XX	Staphylococcus aureus protein; ribozyme; antisense sequence; control;	
KW	Staphylococcal gene; regulatory element; bacterial gene expression;	
KM	vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome;	
KX	toxic shock syndrome.	
OS	Staphylococcus aureus.	
XX		
XX	Key Location/Qualifiers	
FT	Misc-difference 1..89	
FT	/note= "residues designated X are not defined in	
FT	the specification"	
FT	Misc-difference 50	
FT	/note= "encoded by GGN"	
XX		
XX	W09730070-A1.	
XX	21-AUG-1997.	
XX		
XX	19-FEB-1997; 97WO-US02318.	
XX		
XX	20-FEB-1996; 96US-0011888.	
XX		
XX	(SMIK ) SMITHKLINE BEECHAM CORP.	
XX		
PI	Black MT, Burnham MK, Hodgson JE, Knowles DJC, Nicholas RO;	
PI	Pratt JM, Reichard RW, Rosenberg M, Ward JM;	
DR	WPI; 1997-424966/39.	
DR	N-PSDB; AAT83750.	
XX		
PT	Novel, polypeptide(s) from Staphylococcus aureus strain WCUH29 - used	
PT	to isolate antimicrobial compounds, and in vaccines against S.	
PT	aureus infection	
XX		
XX	Claim 6; Page 271; 989pp; English.	
XX		
XX	The present sequence represents a Staphylococcus aureus protein, that,	
CC	based on homology with an Escherichia coli protein, is believed to be an	
CC	outer membrane protein F precursor. The DNA sequence was isolated from a	
CC	library of clones of S. aureus WCUH 29 in Escherichia coli. The DNA	
CC	sequence can be used in the construction of ribozymes and antisense	
CC	sequences to control the expression of staphylococcal genes. The DNA	
CC	sequence is also useful as a source of regulatory elements for the	
CC	control of bacterial gene expression. The present protein may be used	
CC	to produce vaccines to enable a host to produce specific antibodies	
CC	with antibacterial action. These vaccines and antibodies would protect	
CC	a host against invasion by S. aureus, and conditions relating to	
CC	Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled	
CC	skin syndrome, and toxic shock syndrome.	
XX		
XX	Sequence 89 AA;	
XX		
Query Match	11.6%; Score 226.5; DB 18; Length 89;	
Best Local Similarity	59.2%; Pred No. 3.6e-11;	

[illegible]

[illegible]

RESULT	12
AAp90098	
ID	AAp90098 standard; protein; 362 AA.

AC	AAP90098;
XX	
DT	01-NOV-1989 (first entry)
XX	
DE	P2 antigen of Haemophilus influenzae.
XX	
KW	Haemophilus influenzae P2 antigen; vaccines; pathogenic type b strains.
XX	
OS	Haemophilus influenzae type b.
XX	
PN	EP320289-A.
PD	14-JUN-1989.
XX	
PF	09-DEC-1988; 88EP-0311691.
XX	
PR	10-DEC-1987; 87US-0249482.
XX	
PA	--- (TEXA ) UNIV OF TEXAS SYST.
PI	Hansen EJ;
XX	
DR	WPI; 1989-174562/24.
XX	
PT	DNA encoding Haemophilus influenzae P2 antigen - used for producing immunogenic compns. as vaccines and in diagnostic hybridisation assays.
XX	
PS	Disclosure; fig 6; 20pp; English.
XX	
CC	P2 antigen of Haemophilus influenzae (see corresp. AAN90033).
CC	Isolated from type b strains; the P2 antigens are used as vaccines
CC	and to detect P2-specific RNA or DNA. Segments used as antigens
CC	include amino acids 21-361, 175-197, 260-275, 296-311, 33-353,
CC	or their functional equivalents.
XX	
50	Sequence 362 AA;

Query Match	9.0%;	Score 176;	DB 10;	Length 362;
Best Local Similarity	24.1%;	Pred. No. 2.5e-06;		
Matches	90;	Conservative 53;	Mismatches 145;	Indels 86;
				Gaps 16;

QY 4 KVALLIPALLAAGAHAAEVYNKDGKIDL YGKVDGLHYFSNKKDVSDQTY----- 56

Db 3 ktlaalivgafaasanaavynnegtivelgrlllaeqsinstvdnqkqghalrnq 62

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0Y 57 -MRGFKGZTOVDTDLTGQGMEXQIQGNSXENNNNSW----TFVAFAGLKFQDVSFDDY 11L
Db 63 gsrflhkaclhmfgdgIyaqgylectfvcasemsamfgdatskyayvlltgnkafgevkI 122
0Y 112 GRNYGVVVDVTSWTEVLEPEFGDFTYGSNDPMEQQRGN-FGATYRNTDPEFGLVDGILNFAVQY 170
Db 123 graktiagdtisaed--keyg--vImnsdyIptsgntcvyrtfkId--glvlgany---- 172
0Y 171 OGKNCNPSEGEFTSGVTNNGRDALRQNGDVGGSITYDYEGFGIGAISSSKRTDAONTA 230
Db 173 -----llaqreggkq-----enkrpndkage 194
0Y 231 AYIG---NGBRAETTYGGLKTDANNITYLAAYOTF---YNA TRYGSLGMANKAO--NFEA 282
Db 195 vrlgltmgldqy-----gakydandivakliaygrtynklyhesd-----bhkqglngvla 243
0Y 283 VAQYQF-DFGLRPLSIAYIQSGSKNMLNGRCYDDEDDILKTVVDGATYFENKKNSTYDYRI-- 339
Db 244 tlygftsdglilvlsdgsyaktynklykhekr---yIvpspfyqelmedtnvgnfkfyer 300
0Y 340 NLLDDNOFTDAGI 353
Db 301 tsvdgdgktrqgav 314

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RESULT	13
AAV26024	
ID	AAV26024 standard; Protein; 343 AA.

AC	AAY26024;
XX	
DT	29-SEP-1999 (first entry)

DE ompH protein of *Pasteurella multocida* P-1059;  
XX  
XX Outer membrane protein H; ompH gene; fowl cholera; molecular sieve  
KW *Pasteurella multocida* P-1059; porin; vaccine; veterinary medicine;  
KW bacterial porin; *B. influenzae* porin P2; avian.  
XX  
XX *Pasteurella multocida*.  
DS

FT	Key	Location/Qualifiers
FT	Peptide	1..20
FT		/label="Signal_peptide
FT		/note="Hydrophobic amino acids"
FT	Protein	21..343
FT		/note="mature Omph protein"
FT	Cleavage-site	7..9
FT		"Found within signal_peptide"
FT	Cleavage-site	9..11
FT		"Found within signal_peptide"
FT	Cleavage-site	12..14
FT		"Found within signal_peptide"
FT	Cleavage-site	18..20
FT		"Found within signal_peptide"

PN	MO9929724-A2.	
XX		
PD	17-JUN-1999.	
XX		
PF	08-DEC-1998;	98MO-US25990
XX		
XX		
PR	21-JUL-1998;	98US-0120051
PR	08-DEC-1997;	97US-0067957

PA (UYGE-) UNIV GEORGIA RES FOUND INC.

PI Glisson JR, Luo Y;

DR WPI; 1999-385575/32.  
DR N-PSDB; AAX80610.

PT DNA encoding *Pasteurella multocida* outer membrane protein H, useful



